

Adrian

MUSE (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Msrch_p protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Jun 19 15:54:15 2000; Maspar time 5.82 Seconds
Tabular output not generated. 325.701 Million cell updates/sec

Title: >US-09-142-524A-1
Description: (1-80) from US09142524A.pep
Perfect Score: 569
Sequence: 1 MKVTVAFOGPNRRVFIKR.....IASRRVDGIIAAYONPASMK 80

Scoring table: PAM 150
Gap 11

Searched: 188963 segs, 23686106 residues

Post-processing: Minimum Match 08
Listing first 45 summaries

Database: a.geneseg3
1.genesegp

Statistics: Mean 27.708; Variance 116.071; scale 0.239

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	Pred. No.
1	569	100.0	80	1 W27369	Multi-epitope peptide	5.38e-45
2	372	65.4	105	1 W27370	Multi-epitope peptide	1.34e-25
3	372	65.4	134	1 W27371	Multi-epitope peptide	1.34e-25
4	129	22.7	460	1 R6791	Japanese cedar pollen	6.23e-03
5	129	22.7	514	1 R53690	Japanese cedar pollen	6.23e-03
6	129	22.7	514	1 R74333	Japanese cedar pollen	6.23e-03
7	129	22.7	514	1 R93599	Japanese cedar pollen	6.23e-03
8	129	22.7	514	1 R69792	Japanese cedar pollen	6.23e-03
9	129	22.7	514	1 R81586	Japanese cedar pollen	6.23e-03
10	128	22.5	47	1 W80357	Sugi pollen allergen	7.58e-03
11	117	20.6	17	1 W80347	Sugi pollen allergen	6.45e-02
12	117	20.6	33	1 W80339	Sugi pollen allergen	6.45e-02
13	115	20.2	17	1 W80345	Sugi pollen allergen	2.03e-01
14	111	19.5	17	1 W80345	Sugi pollen allergen	2.03e-01
15	111	19.5	17	1 R81580	Sugi pollen allergen	2.03e-01
16	107	18.8	15	1 W57760	Japanese cedar pollen	4.34e-01
17	107	18.8	15	1 W57760	Japanese cedar pollen	4.34e-01
18	107	18.8	47	1 W80350	Sugi pollen allergen	4.34e-01
19	106	18.1	47	1 W80356	Sugi pollen allergen	5.24e-01
20	103	16.1	35	1 W80342	Sugi pollen allergen	9.20e-01
21	98	17.2	15	1 W57764	Residues 186-200 of Cr	2.33e+00
22	98	17.2	15	1 R97908	Residues 186-200 of Cr	2.33e+00
23	98	17.2	15	1 R97907	Japan cedar pollen mat	2.33e+00

ID	Score	Query Match	Length	DB ID	Description	Pred. No.
24	98	17.2	15	1 W57763	Residues 181-195 of Cr	2.33e+00
25	97	17.0	30	1 R45588	Cry j I pollen allergen	2.80e+00
26	97	17.0	354	1 W04344	Chamaecyparis obtusa p	2.80e+00
27	97	17.0	354	1 W42121	Japanese cypress polle	2.80e+00
28	97	17.0	375	1 W04345	Chamaecyparis obtusa p	2.80e+00
29	97	17.0	514	1 W04346	Japanese cypress polle	2.80e+00
30	97	17.0	514	1 W42122	Residues 211-225 of Cr	4.03e+00
31	95	16.7	15	1 W57755	Japanese cedar pollen	4.03e+00
32	95	16.7	15	1 R89293	Sugi pollen allergen	4.03e+00
33	95	16.7	17	1 W80349	Sugi pollen allergen	4.03e+00
34	95	16.7	20	1 R45563	Cry j I pollen allergen	4.03e+00
35	95	16.7	26	1 R82512	Cry j I pollen allergen	4.03e+00
36	95	16.7	28	1 R45594	Cry j I pollen allergen	4.03e+00
37	95	16.7	30	1 W44687	T-cell epitope peptide	4.03e+00
38	95	16.7	353	1 R75388	Japanese cedar pollen	4.03e+00
39	95	16.7	367	1 R45577	Jun s I pollen allergen	4.03e+00
40	95	16.7	374	1 R45541	Cry j I pollen allergen	4.03e+00
41	95	16.7	374	1 R60166	Japanese cedar pollen	4.03e+00
42	95	16.7	374	1 R31937	Sequence encoded by a	4.03e+00
43	95	16.7	680	1 R34445	Human KAL protein.	4.03e+00
44	95	16.7	680	1 W49015		4.03e+00

ALIGNMENTS

RESULT 1
ID W27369 standard; peptide; 80 AA.
AC W27369;

DE Multi-epitope peptide used as immunotherapeutic agent #1.
KW Multi-epitope peptide; immunotherapeutic agent; allergic disease;
T-cell epitope region; allergen; lymphocyte; immunoglobulin E.
OS Synthetic.
PN W09732600-A1.
PD 12-SEP-1997.
PE 10-MAR-1997; J00740.
PR 10-MAR-1996; JP-080702.
PA (MEIP) MEIJI MILK PROD CO LTD.
PI Daiichi K, Iwama A, Kuno K, Kume A, Sone T;
DR WPI: 97-470495/43.
PT Peptide immuno:therapeutic agent to treat allergic diseases -
PT contains multi-epitope peptide containing T cell epitope regions
PT from different allergens
PS Claim 6; Page 31; 58pp; Japanese.
CC The present sequence represents a multi-epitope peptide which is used as
CC or more different allergens (preferably linked via arginine or lysine
CC dimers), where the T cell epitope regions have a positivity index
CC greater than 100 as measured in a patient group responding to the
CC allergen; have at least 70% reactivity with lymphocytes from patients
CC responding to the allergen; and are not reactive with immunoglobulin E
CC (IgE) antibodies from patients responsive to the allergen. The agent can
CC be used to prevent and treat a wide variety of allergic diseases, e.g. by
CC desensitisation. Side effects, e.g. those mediated by IgE, are reduced.
SQ Sequence 80 AA;

APP15.PCT

Query Match 100.0%; Score 569; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 5.38e-45;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 1 MKVTVAFOGPNRRVFIKRVSNTIIGRIDIFASKNFKHLOKNTIGRRISLTSKG 60
QY 1 MKVTVAFOGPNRRVFIKRVSNTIIGRIDIFASKNFKHLOKNTIGRRISLTSKG 60
Db 61 IASRRVDGIIAAYONPASMK 80
QY 61 IASRRVDGIIAAYONPASMK 80
RESULT 2
ID W27370 standard; peptide; 105 AA.
AC W27370;

24-MAR-1998 (first entry)
 DE Multi-epitope peptide used as immunotherapeutic agent #2.
 KW Multi-epitope peptide; immunotherapeutic agent; allergic disease;
 T-cell epitope region; allergen; lymphocyte; immunoglobulin E.
 OS Synthetic.
 PN WO9732600-A1.
 PD 12-SEP-1997.
 PF 10-MAR-1997; J00740.
 PR 10-MAR-1996; JP-080702.
 PA (MEIP) MEIJI MILK PROD CO LTD.
 PI Dairiki K, Iwama A, Kuno K, Kume A, Sone T;
 DR WPI: 97-470495/43.
 PT Peptide immuno:therapeutic agent to treat allergic diseases -
 PT contains multi-epitope peptide containing T cell epitope regions
 from different allergens
 PS Claim 6: Page 31: 58pp; Japanese.
 CC The present sequence represents a multi-epitope peptide which is used as
 a new immunotherapeutic agent. It comprises T cell epitope regions from 2
 or more different allergens (preferably linked via arginine or lysine
 dimers), where the T cell epitope regions have a positively index
 greater than 100 as measured in a patient group responding to the
 allergen: have at least 70% reactivity with lymphocytes from patients
 CC responding to the allergen: and are not reactive with immunoglobulin E
 CC (IgE) antibodies from patients responsive to the allergen. The agent can
 be used to prevent and treat a wide variety of allergic diseases, e.g. by
 desensitisation. Side effects, e.g. those mediated by IgE, are reduced.
 CC Sequence 105 AA;

Query Match 65.4%; Score 372; DB 1; Length 105;
 Best Local Similarity 100.0%; Pred. No. 1.34e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MKVTVAENFGPNRRVFIRKRVSNVTHGRRIDIFASKNFHLQKNTIGTGR 51
 QY 1 MKVTVAENFGPNRRVFIRKRVSNVTHGRRIDIFASKNFHLQKNTIGTGR 51

RESULT 3
 ID W27371 standard; peptide: 134 AA.
 AC W27371;
 DT 24-MAR-1998 (first entry)
 DE Multi-epitope peptide used as immunotherapeutic agent #3.
 KW Multi-epitope peptide; immunotherapeutic agent; allergic disease;
 T-cell epitope region; allergen; lymphocyte; immunoglobulin E.
 OS Synthetic.
 PN WO9732600-A1.
 PD 12-SEP-1997.
 PF 10-MAR-1997; J00740.
 PR 10-MAR-1996; JP-080702.
 PA (MEIP) MEIJI MILK PROD CO LTD.
 PI Dairiki K, Iwama A, Kuno K, Kume A, Sone T;
 DR WPI: 97-470495/43.
 PT Peptide immuno:therapeutic agent to treat allergic diseases -
 PT contains multi-epitope peptide containing T cell epitope regions
 from different allergens
 PS Claim 6: Page 32: 58pp; Japanese.
 CC The present sequence represents a multi-epitope peptide which is used as
 a new immunotherapeutic agent. It comprises T cell epitope regions from 2
 or more different allergens (preferably linked via arginine or lysine
 dimers), where the T cell epitope regions have a positively index
 greater than 100 as measured in a patient group responding to the
 allergen: have at least 70% reactivity with lymphocytes from patients
 CC responding to the allergen: and are not reactive with immunoglobulin E
 CC (IgE) antibodies from patients responsive to the allergen. The agent can
 be used to prevent and treat a wide variety of allergic diseases, e.g. by
 desensitisation. Side effects, e.g. those mediated by IgE, are reduced.
 CC Sequence 134 AA;

Query Match 65.4%; Score 372; DB 1; Length 134;
 Best Local Similarity 100.0%; Pred. No. 1.34e-25;
 Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MKVTVAENFGPNRRVFIRKRVSNVTHGRRIDIFASKNFHLQKNTIGTGR 51

QY 1 MKVTVAENFGPNRRVFIRKRVSNVTHGRRIDIFASKNFHLQKNTIGTGR 51

RESULT 4
 ID R69791 standard; Protein: 460 AA.
 AC R69791;
 DT 27-SEP-1995 (first entry)
 DE Japonicum allergen residues 55-514.
 KW Japonicum allergen; residues 55-514; induced histamine release;
 T cell allergic peptide; IgE cross-linking inhibition.
 OS Japonicum sp.
 PN WO9502412-A.
 PD 26-JAN-1995.
 PF 15-JUL-1994; J01164.
 PR 16-JUL-1993; JP-177008.
 PR 01-SEP-1993; JP-217725.
 PR 07-APR-1994; JP-069336.
 PA (MEIP) MEIJI MILK PROD CO LTD.
 PI Kuno K, Kohno Y, Komiyama N, Sone T;
 DR WPI: 95-067159/09.
 DR N-PSDB; Q84044.
 PT Peptide anti-allergic agent - inhibits cross-linking of allergen
 with IgE antibody
 PS Disclosure; Pages 26-27; 46pp; Japanese.
 CC Q84044 encodes R69791 Japonicum allergen residues 55-514, from
 CC which the anti-allergic peptides R69845-R69809 were derived.
 CC The peptides ability to inhibit the cross-linking of an allergen,
 CC to an IgE antibody can be used in the prevention and treatment of
 CC allergic diseases.
 CC Sequence 460 AA;

Query Match 22.7%; Score 129; DB 1; Length 460;
 Best Local Similarity 100.0%; Pred. No. 6.23e-03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 182 IDIFASKNFHLQKNTIGTG 200
 QY 31 IDIFASKNFHLQKNTIGTG 49

RESULT 5
 ID R53690 standard; Protein: 514 AA.
 AC R53690;
 DT 01-FEB-1995 (first entry)
 DE Japanese cedar pollen allergen Cry j II.
 KW Cedar pollinosis; diagnostic.
 OS Cryptomeria japonica.
 PN WO9411512-A.
 PD 26-MAY-1994.
 PF 12-NOV-1993; U11000.
 PR 12-NOV-1992; US-975179.
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 PI Brauer A, Kuo M, Pollock J, Yeung S;
 DR WPI: 94-183513/22.
 DR N-PSDB; Q66048.
 PT Allergenic Cry j II protein and fragments from Japanese cedar
 PT pollen - used to diagnose, treat and prevent Japanese cedar
 PT pollinosis
 PS Claim 2: Fig 4; 89pp; English.
 CC The sequence is of a Japanese cedar pollen allergen Cry j
 CC II. The protein and its fragments can be used for diagnosis and
 CC treatment of Japanese cedar pollinosis and to identify similar
 CC sequences in other plants.
 CC See also R53692-6.
 CC Sequence 514 AA;

Query Match 22.7%; Score 129; DB 1; Length 514;
 Best Local Similarity 100.0%; Pred. No. 6.23e-03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 182 IDIFASKNFHLQKNTIGTG 254

Query 31 IDIFASKNFHLQKNTIGTG 49

RESULT 6
ID R74333 standard; Protein; 514 AA.
AC R74333;
DE 01-NOV-1995 (first entry)
KW Japanese cedar pollen allergen.
KW Japanese cedar pollen allergen; allergy; therapy; diagnostic;
KW desensitizer.
OS Cryptomeria japonica.
PN EP-655500-A.
PD 31-MAY-1995.
PE 03-NOV-1994; 308117.
PR 05-NOV-1993; JP-299151.
PR 20-DEC-1993; JP-344596.
PR 27-DEC-1993; JP-346814.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI Kurimoto M, Namba M, Torioge K;
DR WPI; 95-195588/26.
DR N-PSDB; 090156.
PT New Japanese cedar pollen allergen polypeptide - and DNA coding for it,
PT useful for treatment and diagnosis of cedar pollen allergy
PS Claim 5; Page 26-28; 41pp; English.
CC The gene encoding an allergen of Japanese cedar pollen was isolated
CC by PCR amplification using primers based on portions of the allergen
CC protein. The gene was used for recombinant allergen production in
CC E. coli (vector plasmid pKK-223-3).
SQ Sequence 514 AA;

Query Match 22.7%; Score 129; DB 1; Length 514;
Best Local Similarity 100.0%; Pred. No. 6.23e-03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 236 IDIFASKNFHLQKNTIGTG 254
Query 31 IDIFASKNFHLQKNTIGTG 49

RESULT 7
ID R93599 standard; Protein; 514 AA.
AC R93599;
DE 16-AUG-1996 (first entry)
KW Japan cedar pollen Cry j II allergen.
KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
KW Sugi pollinosis; diagnosis; treatment.
OS Cryptomeria japonica.
FH Key location/Qualifiers
FT peptide 1..54
FT /*label= sig_peptide
FT /*label= 55..514
FT /*label= mat_protein
PD J08047392-A.
PD 20-FEB-1996.
PD 07-NOV-1994; 297840.
PR 05-NOV-1993; JP-276773.
PR 26-MAY-1994; JP-134868.
PA (MEIP) MEIJI MILK PROD CO LTD.
DR WPI; 96-166249/17.
DR N-PSDB; T18102.
PT Japan cedar pollen allergen Cry j II epitope - comprises at least
PT part of specified 460 amino acid protein
PS Claim 1; Page 10-11; 17pp; Japanese.
CC R93599 is a Japan cedar pollen Cry j II allergen which is useful
CC in the diagnosis, prevention and treatment of Sugi pollinosis,
CC the allergic reaction to Japan cedar pollen. Significant regions of
CC the allergen were identified using overlapping peptides of the full
CC epitope derived from a Cry j II antigen-specific T cell line
CC (see R9781-1-997960). Amino acids 66-80 (R97884) and 186-200 (R978908)
CC of the full mature 460 amino acid allergen are the most allergenic
CC of the 90 peptides tested.
SQ Sequence 514 AA;

Query Match 22.7%; Score 129; DB 1; Length 514;
Best Local Similarity 100.0%; Pred. No. 6.23e-03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 236 IDIFASKNFHLQKNTIGTG 254
Query 31 IDIFASKNFHLQKNTIGTG 49

RESULT 8
ID R69792 standard; Protein; 514 AA.
AC R69792;
DE 27-SEP-1995 (first entry)
KW Japonicum allergen.
KW Japonicum allergen; induced histamine release; antiallergic peptide;
KW Ige cross-linking inhibition.
OS Japonicum sp.
PN WO9502412-A.
PD 26-JAN-1995.
PE 15-JUL-1994; J01164.
PR 16-JUL-1993; JP-177008.
PR 01-SEP-1993; JP-217725.
PR 07-APR-1994; JP-069336.
PA (MEIP) MEIJI MILK PROD CO LTD.
PI Kino K, Kohno Y, Komiyama N, Sone T;
DR WPI; 95-067159/09.
DR N-PSDB; 084045, 084046.
PT Peptide anti-allergic agent - inhibits cross-linking of allergen
PT with Ige antibody
PS Example 3; Pages 27-28; 46pp; Japanese.
CC 084045 encodes R69792 Japonicum allergen, from which the antiallergic
CC peptides R69845-R69809 were derived. The peptides ability to inhibit
CC the cross-linking of an allergen, to an Ige antibody can be used in
CC the prevention and treatment of allergic diseases.
SQ Sequence 514 AA;

Query Match 22.7%; Score 129; DB 1; Length 514;
Best Local Similarity 100.0%; Pred. No. 6.23e-03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 236 IDIFASKNFHLQKNTIGTG 254
Query 31 IDIFASKNFHLQKNTIGTG 49

RESULT 9
ID R81586 standard; Protein; 514 AA.
AC R81586;
DE 24-MAY-1996 (first entry)
KW Cedar pollen allergen A.
KW Cedar pollen allergen; immunoglobulin E; Ige; T-cell epitope;
KW antibody; pollinosis; therapy; immunotherapy.
OS Cryptomeria japonica.
PN EP-700929-A2.
PD 13-MAR-1996.
PD 08-SEP-1994; 306295.
PR 10-SEP-1994; JP-242137.
PR 14-JUL-1995; JP-200221.
PR 14-JUL-1995; JP-200204.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI Hino K, Saito S, Taniguchi Y;
DR WPI; 96-140976/15.
PT New peptide(s) derived from cedar pollen allergens - activate
PT allergen-specific T-cells, but not allergen-specific Ige antibodies,
PT used for treating cedar pollinosis
PS Claim 5; Page 29-30; 36pp; English.
CC Synthetic peptides based on portions of cedar pollen allergens A
CC (R81586) and B (R81587) were tested for their ability to activate
CC cedar allergen-specific T-cells, but not allergen-specific Ige
CC antibodies. 6 peptides (R81580-R81585) were identified as T-cell
CC epitopes. These peptides, plus subsequences (R81573-79) essential
CC for T-cell recognition, and homologous peptides (R81588-96) can
CC be used as immunotherapeutic agents to treat or prevent cedar

CC pollinosis, avoiding side-effects such as anaphylaxis.
Sequence 514 AA.

Query Match 22.7%; Score 129; DB 1; Length 514;
Best Local Similarity 100.0%; Pred. No. 6,23e-03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 236 IDIFASKNFHLQKNTIGT 254
IDIFASKNFHLQKNTIGT 49

Query Match 22.7%; Score 129; DB 1; Length 514;
Best Local Similarity 100.0%; Pred. No. 6,23e-03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
ID W80357 standard; peptide: 47 AA.

AC W80357:
DE 11-JAN-1999 (first entry)
DE Sugi allergen protein Cryj1 derived epitope for T cells.
KW T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;
KW sugi-pollinosis; allergic reaction; pollen.
OS Synthetic.
PN J10259198-A.
PD 29-SEP-1998.
PF 22-DEC-1997; 353448.
PR 24-DEC-1996; JP-343441.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PA (SANY) SANKYO CO LTD.
DR WPI: 98-577037/49.
PT A linked T cell epitope peptide - used for the treatment of
PT sugi-pollinosis
PS Claim 10; Page 5; 21pp; Japanese.
CC W80339-58 represent epitopes for T cells, derived from the sugi allergen
CC proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345-49
CC and W80354-55). The peptides are useful for the treatment of
CC sugi-pollinosis, an allergic reaction of the body to pollen.
SQ Sequence 47 AA.

Query Match 22.5%; Score 128; DB 1; Length 47;
Best Local Similarity 84.0%; Pred. No. 7,58e-03;
Matches 21; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

Db 12 KLTSKRIASC-LNGIIAAYONPASM 35
KLTSKRIASC-LNGIIAAYONPASM 79

RESULT 11
ID W80347 standard; peptide: 17 AA.

AC W80347:
DE 11-JAN-1999 (first entry)
DE Sugi allergen protein Cryj2 derived epitope for T cells.
KW T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;
KW sugi-pollinosis; allergic reaction; pollen.
OS Synthetic.
PN J10259198-A.
PD 29-SEP-1998.
PF 22-DEC-1997; 353448.
PR 24-DEC-1996; JP-343441.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PA (SANY) SANKYO CO LTD.
DR WPI: 98-577037/49.
PT A linked T cell epitope peptide - used for the treatment of
PT sugi-pollinosis
PS Claim 7; Page 18; 21pp; Japanese.
CC W80339-58 represent epitopes for T cells, derived from the sugi allergen
CC proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345-49
CC and W80354-55). The peptides are useful for the treatment of
CC sugi-pollinosis, an allergic reaction of the body to pollen.
SQ Sequence 17 AA.

Query Match 20.6%; Score 117; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 6,45e-02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 IDIFASKNFHLQKNTIG 17
IDIFASKNFHLQKNTIG 47

Query Match 22.7%; Score 129; DB 1; Length 514;
Best Local Similarity 100.0%; Pred. No. 6,23e-03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 236 IDIFASKNFHLQKNTIGT 254
IDIFASKNFHLQKNTIGT 49

Query Match 22.7%; Score 129; DB 1; Length 514;
Best Local Similarity 100.0%; Pred. No. 6,23e-03;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
ID W80357 standard; peptide: 47 AA.

AC W80357:
DE 11-JAN-1999 (first entry)
DE Sugi allergen protein Cryj1 derived epitope for T cells.
KW T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;
KW sugi-pollinosis; allergic reaction; pollen.
OS Synthetic.
PN J10259198-A.
PD 29-SEP-1998.
PF 22-DEC-1997; 353448.
PR 24-DEC-1996; JP-343441.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PA (SANY) SANKYO CO LTD.
DR WPI: 98-577037/49.
PT A linked T cell epitope peptide - used for the treatment of
PT sugi-pollinosis
PS Claim 10; Page 5; 21pp; Japanese.
CC W80339-58 represent epitopes for T cells, derived from the sugi allergen
CC proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345-49
CC and W80354-55). The peptides are useful for the treatment of
CC sugi-pollinosis, an allergic reaction of the body to pollen.
SQ Sequence 47 AA.

Query Match 20.6%; Score 117; DB 1; Length 33;
Best Local Similarity 67.7%; Pred. No. 6,45e-02;
Matches 21; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Db 1 FASKNFHLQKNTIGT-RRISKLTSKRIAS 31
FASKNFHLQKNTIGT-RRISKLTSKRIAS 63

RESULT 13
ID R81582 standard; peptide: 17 AA.

AC R81582:
DE 24-MAY-1996 (first entry)
DE Cedar pollen allergen peptide 10 (T-cell epitope).
KW Cedar; Cryptomeria japonica; pollen; allergen; immunoglobulin E;
KW IGE; T-cell epitope; antibody; pollinosis; therapy; immunotherapy.
OS Synthetic.
PN EP-700929-A2.
PD 13-MAR-1996.
PF 08-SEP-1995; 306295.
PR 10-SEP-1994; JP-242137.
PR 14-JUL-1995; JP-200221.
PR 14-JUL-1995; JP-200204.
PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PA Hino K. Saito S. Taniguchi Y;
DR WPI: 96-140976/15.
PT New peptide(s) derived from cedar pollen allergens - activate
PT allergen-specific T-cells, but not allergen-specific IGE antibodies,
PT used for treating cedar pollinosis
PS Claim 4; Page 28; 36pp; English.
CC Synthetic peptides based on portions of cedar pollen allergens A
CC (R81586) and B (R81587) were tested for their ability to activate
CC cedar allergen-specific T-cells, but not allergen-specific IGE
CC antibodies. 6 peptides (R81580-R81585) were identified as T-cell
CC epitopes. These peptides, plus subsequences (R81573-79) essential
CC for T-cell recognition, and homologous peptides (R81588-96) can
CC be used as immunotherapeutic agents to treat or prevent cedar
CC pollinosis, avoiding side-effects such as anaphylaxis.
SQ Sequence 17 AA.

Query Match 20.2%; Score 115; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 9,47e-02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 DIFASKNFHLQKNTIGT 17
 OY 32 DIFASKNFHLQKNTIGT 48

RESULT 14

ID W80345 standard; peptide; 17 AA.
 AC W80345;
 DT 11-JAN-1999 (first entry)
 DE Sugi1 allergen protein Cryj2 derived epitope for T cells.
 KW T cell epitope; sugi1 allergen proteins Cryj1; Cryj2; treatment;
 OS Sugi1-pollinosis; allergic reaction; pollen.
 PN 110259198.A.
 PD 29-SEP-1998.
 PE 22-DEC-1997; 353448.
 PR 24-DEC-1996; JP-343441.
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PA (SANY) SANKYO CO LTD.
 DR WPI: 98-577037/49.
 PT A linked T cell epitope peptide - used for the treatment of
 PT Sugi1-pollinosis
 PS Claim 7; Page 18; 21pp; Japanese.
 CC W80339-58 represent epitopes for T cells, derived from the sugi1 allergen
 CC proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345-49
 CC and W80354-55). The peptides are useful for the treatment of
 CC Sugi1-pollinosis, an allergic reaction of the body to pollen.
 SQ Sequence 17 AA;

Query Match

Best Local Similarity 93.8%; Score 111; DB 1; Length 17;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 KVDGIITAYONPASWK 16
 OY 65 RVDGIITAYONPASWK 80

RESULT 15

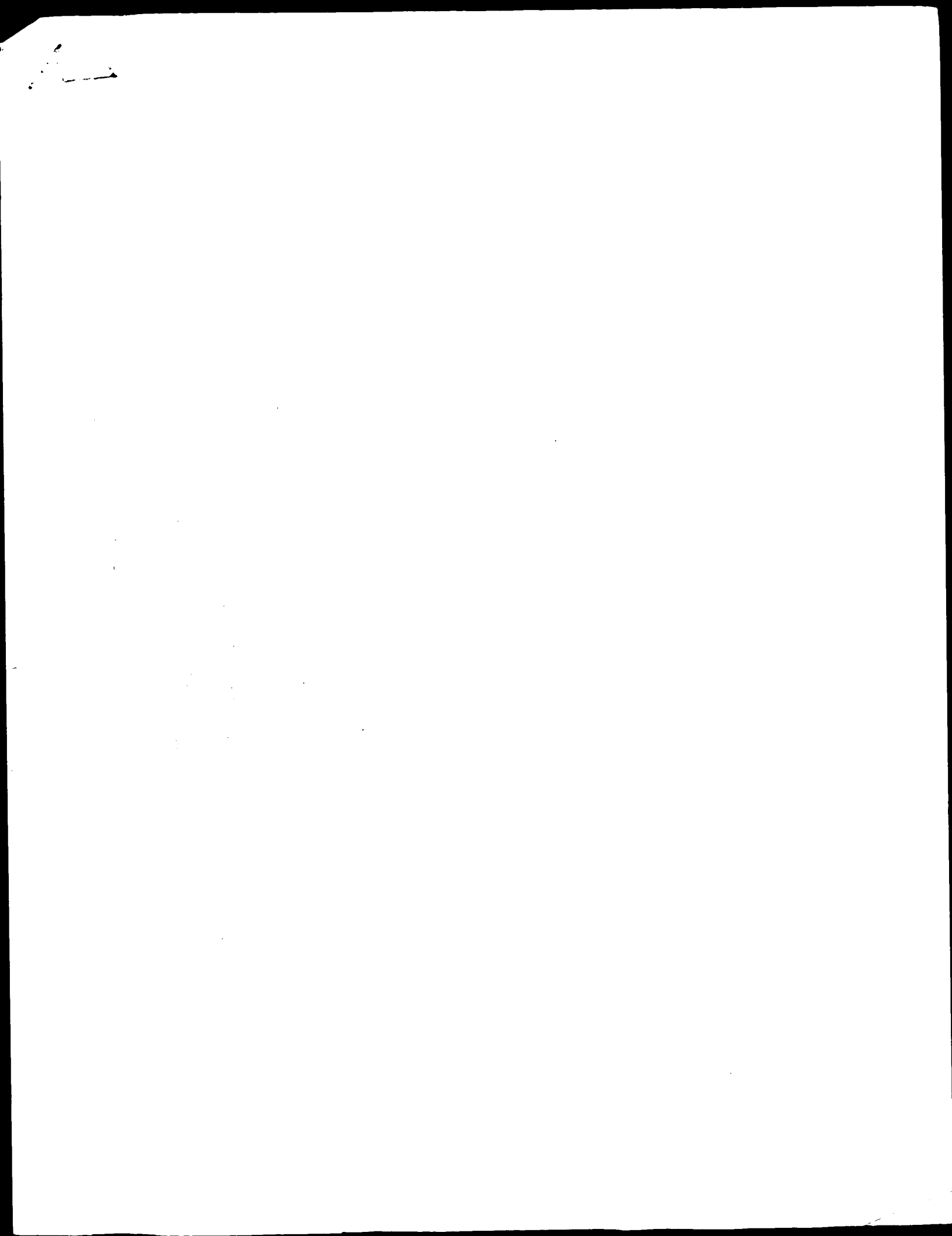
ID R81580 standard; Peptide; 17 AA.
 AC R81580;
 DT 24-MAY-1996 (first entry)
 DE Cedar pollen allergen peptide 8 (T-cell epitope).
 KW Cedar; Cryptomeria japonica; pollen; allergen; immunoglobulin E;
 KW IgE; T-cell epitope; antibody; pollinosis; therapy; immunotherapy.
 OS Synthetic
 PN EP-700929-A2.
 PD 13-MAR-1996.
 PE 08-SEP-1995; 306295.
 PR 10-SEP-1994; JP-242137.
 PR 14-JUL-1995; JP-200221.
 PR 14-JUL-1995; JP-200204.
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Hino K, Saito S, Taniguchi Y;
 DR WPI: 96-140976/15.
 PT New peptide(s) derived from cedar pollen allergens - activate
 PT allergen-specific T-cells, but not allergen-specific IgE antibodies,
 PT used for treating cedar pollinosis
 PS Claim 4; Page 28; 36pp; English.
 CC Synthetic peptides based on portions of cedar pollen allergens A
 CC (R81586) and B (R81587) were tested for their ability to activate
 CC cedar allergen-specific T-cells, but not allergen-specific IgE
 CC antibodies. 6 Peptides (R81580-R81585) were identified as T-cell
 CC epitopes. These peptides, plus subsequences (R81573-78) essential
 CC for T-cell recognition, and homologous peptides (R81588-96) can
 CC be used as immunotherapeutic agents to treat or prevent cedar
 CC pollinosis, avoiding side-effects such as anaphylaxis.
 SQ Sequence 17 AA;

Query Match

Best Local Similarity 93.8%; Score 111; DB 1; Length 17;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 KVDGIITAYONPASWK 16
 OY 65 RVDGIITAYONPASWK 80

Search completed: Mon Jun 19 15:54:24 2000
 Job time : 9 secs.



RESULT 2
ENTRY S48730 #type complete
TITLE Cry j II protein - Japanese cedar
#formal_name Cryptomeria japonica #common_name Japanese cedar
ORGANISM 07-May-1995 #sequence_revision 21-Jul-1995 #text_change
DATE 28-May-1999
S48730
ACCESSIONS S48730
REFERENCE Nambu, M.; Kurose, M.; Toriige, K.; Hino, K.; Taniguchi, Y.;
#authors Fukuda, S.; Usui, M.; Kurimoto, M.
#journal FEBS Lett. (1994) 353:124-128
#title Molecular cloning of the second major allergen, Cry j II,
from Japanese cedar pollen.
#cross-references MIMD:95010777
#accession S48730
#status Preliminary
#molecule_type mRNA
#residues 1-514 #label NAM
#cross-references GB:DJ7765; NID:9577695; PIDN:BA07021.1;
PID:d1007598; PID:9577696
SUMMARY #length 514 #molecular_weight 56645 #checksum 586
Query Match 22.7% Score 129; DB 2; Length 514;
Best Local Similarity 100.0%; Pred. No. 4,79e-06;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 236 IDIFASKNFHLQKNTIGT 254
|||
Qy 31 IDIFASKNFHLQKNTIGT 49
RESULT 3
ENTRY S62737 #type complete
TITLE DNA topoisomerase I - Thermotoga maritima (strain MS8)
#formal_name Thermotoga maritima
ORGANISM 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change
DATE 29-Sep-1999
S62737; A72400
ACCESSIONS S62737
REFERENCE Boutlier de la Tour, C.; Kaltoun, H.; Portemer, C.;
#authors Confalonieri, F.; Hubert, R.; Duquet, M.
#journal Biochim. Biophys. Acta (1995) 1264:279-283
#title Cloning and sequencing of the gene coding for topoisomerase I
from the extremely thermophilic eubacterium, Thermotoga
maritima.
#cross-references MIMD:96138548
#accession S62737
#status Preliminary
#molecule_type DNA
#residues 1-633 #label BOU
#cross-references EMBL:U27841; NID:9881493; PIDN:AAA68949.1;
PID:9881494
REFERENCE A72200
#authors Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson,
R.J.; Heft, D.H.; Hickey, E.K.; Peterson, J.D.; Nelson,
W.C.; Ketchum, K.A.; McDonald, L.; Uterback, T.R.; Malek,
J.A.; Linher, K.D.; Garrett, M.M.; Stewart, A.M.; Cotton,
M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
Heidelberg, J.; Sutton, G.G.; Fleischmann, R.D.; White, O.;
Salzberg, S.L.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
#journal Nature (1999) 399:323-329
#title Evidence for lateral gene transfer between Archaea and
Bacteria from genome sequence of Thermotoga maritima.
#cross-references MIMD:99287316
#accession A72400
#molecule_type DNA
#residues 1-633 #label ARN
#cross-references GB:AE001708; GB:AE000512; NID:94980740; PID:94980754;
TIGR:TM0258
#experimental_source strain MSB8
GENETICS
#gene TM0258

CLASSIFICATION #superfamily DNA topoisomerase I
SUMMARY #length 633 #molecular_weight 72694 #checksum 9092
Query Match 17.2% Score 98; DB 2; Length 633;
Best Local Similarity 26.6%; Pred. No. 1,40e-01;
Matches 17; Conservative 18; Mismatches 26; Indels 3; Gaps 3;
Db 96 IARTNLGKRNRI-VSELTPIRYEAVKPNPREIDKKVRAOLA-RIIDRIYGLSLP 153
|||
Qy 18 IKRNVNTHGRIDIFASKNFHLQKNTIGTRISIKLSGKIASRVDCIIAAVQ-NP 76
Db 154 VLWR 157
Qy 77 ASWK 80
RESULT 4
ENTRY S53913 #type complete
TITLE FKX2 protein - yeast (Saccharomyces cerevisiae)
#formal_name N2403; protein YNL068c
ORGANISM 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change
DATE 24-Sep-1999
ACCESSIONS S53913; S59726; S63000; S62996; S58726; S63942
REFERENCE S53896
#authors Poehlmann, R.; Philippson, P.
#submission submitted to the EMBL Data Library, April 1995
#accession S53913
#molecule_type DNA
#residues 1-862 #label POE
#cross-references EMBL:X86470; NID:9791101; PIDN:CAA60193.1;
PID:9791119
REFERENCE S59725
#authors Zhu, G.; Davis, T.N.
#submission submitted to the EMBL Data Library, January 1995
#description Two fork head homologs in S. cerevisiae.
#accession S59726
#molecule_type DNA
#residues 1-862 #label ZHU
#cross-references EMBL:L38850; NID:9623607; PIDN:AAA60939.1;
PID:9623608
REFERENCE S62997
#authors Poehlmann, R.; Philippson, P.
#submission submitted to the Protein Sequence Database, April 1996
#accession S63000
#molecule_type DNA
#residues 1-862 #label POW
#cross-references EMBL:Z71344; NID:91301948; PIDN:CAA95942.1;
PID:9239903; PID:91301949; MIP:YNL068c
#experimental_source strain S288c
REFERENCE S62975
#authors Berger, P.; Doignon, F.; Crouzet, M.
#submission submitted to the Protein Sequence Database, April 1996
#accession S62996
#molecule_type DNA
#residues 1-440 #label BER
#cross-references EMBL:Z71344; MIP:YNL068c
#experimental_source strain S288c
REFERENCE S58711
#authors Berger, P.; Doignon, F.; Crouzet, M.
#journal Yeast (1995) 11:967-974
#title The sequence of a 44 420 bp fragment located on the left arm
of chromosome XIV from Saccharomyces cerevisiae.
#cross-references MIMD:96021608
#accession S58726
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-440 #label BEW
#cross-references EMBL:U12141; NID:91314216; PIDN:AAA96643.1;
PID:91098481
#note the nucleotide sequence was submitted to the EMBL Data
Library, July 1994
REFERENCE S63925

#authors Poehmann, R.; Philippsen, P.
#journal Yeast (1996) 12:391-402
#title Sequencing a cosmid clone of *Saccharomyces cerevisiae* chromosome XIV reveals 12 new open reading frames (ORFs) and an ancient duplication of six ORFs.
#cross-references MUID:96267764
#accession S63942
#status nucleic acid sequence not shown; translation not shown
#molecule_type DNA
#residues 1-862 #label POE
#cross-references EMBL:X86470; NID:g791101; PIDN:CA60193.1; PID:g791119
#note the nucleotide sequence was submitted to the EMBL Data Library, April 1995
GENETICS SGD:FKH2
#gene #cross-references SGD:S0005012; MIPS:YNL068c
#map_position 14L
CLASSIFICATION #superfamily unassigned fork head proteins; fork head DNA-binding domain homology
FEATURE 340-432
SUMMARY #domain fork head DNA-binding domain homology #label FHD
Query Match 17.0%; Score 97; DB 2; Length 862;
Best Local Similarity 26.7%; Pred. No. 1,90e-01;
Matches 20; Conservative 23; Mismatches 27; Indels 5; Gaps 5;
Db 65 AYAKLSPNMTYYKDL-EVSI-GRNTDPLNS-ALQENSQGVKNYVNTDGPARYVSR 121
Qy 6 AFNPF-GPNRVRFFIKRYSNVTHGRIDIFASKNFHLQKNTIGTGRIISLKLTSKIASR 64
Db 122 K-HAIIYNNNIGW 135
Qy 65 RVDCIIAAYONPASW 79
RESULT 5
ENTRY D48562 #type complete
TITLE hypothetical nucleic acid-binding protein - San Miguel sea lion virus (serotype 4)
ORGANISM #formal_name San Miguel sea lion virus
DATE 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 20-Mar-1998
ACCESSIONS D48562
REFERENCE A48562
#authors Neill, J.D.
#journal Virus Res. (1992) 24:211-222
#title Nucleotide sequence of the capsid protein gene of two serotypes of San Miguel sea lion virus: identification of conserved and non-conserved amino acid sequences among calicivirus capsid proteins.
#cross-references MUID:92410750
#accession D48562
#status preliminary
#molecule_type genomic RNA
#residues 1-110 #label NEI
#cross-references GB:M87482; NID:g334886; PID:g334889
#note sequence extracted from NCBI Backbone (NCBIP:113570)
SUMMARY #length 110 #molecular_weight 12566 #checksum 2707
Query Match 16.7%; Score 95; DB 2; Length 110;
Best Local Similarity 28.9%; Pred. No. 3.50e-01;
Matches 13; Conservative 17; Mismatches 13; Indels 2; Gaps 2;
Db 10 FLNSVANAIVEGKRLDL-ASRGLOLKSALDPERAFNDRALAFK 53
Qy 17 FLKRVSNVTHRRIDIFASKNFHLQKNTIGTGRIISL-KLTSCK 60
RESULT 6
ENTRY JC2124 #type complete
TITLE major allergen Cry j I precursor (clone PCCI-15) - Japanese

ORGANISM cedar
DATE #formal_name Cryptomeria japonica #common_name Japanese cedar
ACCESSIONS 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 26-Aug-1999
REFERENCE JC2124
#authors Sone, T.; Komiyama, N.; Shimizu, K.; Kusakabe, T.; Morikubo, K.; Kino, K.
#journal Biochem. Biophys. Res. Commun. (1994) 199:619-625
#title Cloning and sequencing of cDNA coding for Cry j I, a major allergen of Japanese cedar pollen.
#cross-references MUID:94183234
#accession JC2124
#molecule_type mRNA
#residues 1-374 #label SON
#cross-references GB:D26545; NID:g493633; PID:d1006087; PID:g493634
#experimental_source pollen
#note the authors described carbohydrate binding site for residue 279
CLASSIFICATION #superfamily pectate lyase LAT59
KEYWORDS glycoprotein; pollen
FEATURE 1-21
22-374 #domain signal sequence #status predicted #label SIG
158,191,293,354 #product major allergen Cry j I (clone PCCI-15) #status predicted #label MAR
SUMMARY #binding-site carbohydrate (Asn) (covalent) #status predicted
#length 374 #molecular_weight 40645 #checksum 2920

RESULT 7
ENTRY JC2123 #type complete
TITLE major allergen Cry j I precursor (clone PCCI-2-2) - Japanese cedar
ORGANISM #formal_name Cryptomeria japonica #common_name Japanese cedar
DATE 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 26-Aug-1999
ACCESSIONS JC2123; PC2065
REFERENCE JC2123
#authors Sone, T.; Komiyama, N.; Shimizu, K.; Kusakabe, T.; Morikubo, K.; Kino, K.
#journal Biochem. Biophys. Res. Commun. (1994) 199:619-625
#title Cloning and sequencing of cDNA coding for Cry j I, a major allergen of Japanese cedar pollen.
#cross-references MUID:94183234
#accession JC2123
#molecule_type mRNA
#residues 1-374 #label SON
#cross-references GB:D26544; NID:g493631; PID:d1006086; PID:g493632
#experimental_source pollen
#accession PC2065
#molecule_type protein
#residues 22-53; 58-81; 219-232; 236-258; 299-307; 346-372 #label S02
#note the authors described carbohydrate binding site for residue 279
CLASSIFICATION #superfamily pectate lyase LAT59
KEYWORDS glycoprotein; pollen
FEATURE 1-21
22-374 #domain signal sequence #status predicted #label SIG
158,191,293,354 #product major allergen Cry j I (clone PCCI-2-2) #status predicted #label MAR
SUMMARY #binding-site carbohydrate (Asn) (covalent) #status predicted
#length 374 #molecular_weight 40645 #checksum 2920

Query Match 16.7%; Score 95; DB 2; Length 374;
 Best Local Similarity 100.0%; Pred. No. 3.50e-01;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 234 MKVTVAENQFGPN 246
 1 MKVTVAENQFGPN 13

RESULT 8
 ENTRY A40351 #type complete
 TITLE adhesion-type protein ADMLX - human
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 20-Mar-1998

ACCESSIONS A40351
 REFERENCE A40351
 #authors Legouis, R.; Hardelin, J.P.; Levilliers, J.; Claverie, J.M.; Compain, S.; Wunderle, V.; Millaudeau, P.; Le Paslier, D.; Cohen, D.; Caterina, D.; Bouquelier, L.; Delamarre-Van de Maal, H.; Lutfalla, G.; Weissenbach, J.; Petit, C.

#journal Cell (1991) 67:423-435
 #title The candidate gene for the X-linked Kallmann syndrome encodes a protein related to adhesion molecules.
 #cross-references M0ID:92005720
 #accession A40351

GENETICS #status preliminary
 #molecule-type mRNA
 #residues 1-679 ##label LEG
 #cross-references GB:S60085; NID:g237595; PID:g237597

FEATURES #gene GDB:KAL1, KAL
 #cross-references GDB:120116; OMIM:308700
 #map_position Xp22.32-Xp22.32
 CLASSIFICATION #superfamily antileukoprotease repeat homology
 FEATURE 129-175 #domain antileukoprotease repeat homology #label ALP
 SUMMARY #length 679 #molecular-weight 76301 #checksum 1231

Query Match 16.7%; Score 95; DB 2; Length 679;
 Best Local Similarity 27.1%; Pred. No. 3.50e-01;
 Matches 16; Conservative 19; Mismatches 23; Indels 1; Gaps 1;

Db 247 VQLDTRPSRW-YQFRVAANVHGRTAPSKHFRSSKDPSPAPAPANRLANSTVNS 304
 5 VAFNFGPNRRVFKRVSNIHGRIDIFASKNFHLOKNTIGTRISLKLISGKIAS 63

RESULT 9
 ENTRY S17982 #type complete
 TITLE Kallmann syndrome protein KALIG-1 - human
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 19-Feb-1999

ACCESSIONS S17982
 REFERENCE S17982
 #authors Franco, B.; Guioit, S.; Pragliola, A.; Incerti, B.; Bargon, B.; Tonlorenzi, R.; Carozzo, R.; Maestri, E.; Pieretti, M.; Tallon-Miller, P.; Brown, C.J.; Willard, H.F.; Lawrence, C.; Persico, M.G.; Camerino, G.; Ballabio, A.

#journal Nature (1991) 353:529-536
 #title A gene deleted in Kallmann's syndrome shares homology with neural cell adhesion and axonal path-finding molecules.
 #cross-references M0ID:92018217

#accession S17982
 #status preliminary
 #molecule-type mRNA

GENETICS #residues 1-680 ##label FRA
 #cross-references EMBL:X60299; NID:g34024; PID:g34025

GENETICS GDB:KAL1, KAL
 #gene #cross-references GDB:120116; OMIM:308700
 #map_position Xp22.32-Xp22.32

CLASSIFICATION #superfamily antileukoprotease repeat homology
 FEATURE 130-176 #domain antileukoprotease repeat homology #label ALP
 SUMMARY #length 680 #molecular-weight 76151 #checksum 5161

Query Match 16.7%; Score 95; DB 2; Length 680;
 Best Local Similarity 27.1%; Pred. No. 3.50e-01;
 Matches 16; Conservative 19; Mismatches 23; Indels 1; Gaps 1;

Db 248 VQLDTRPSRW-YQFRVAANVHGRTAPSKHFRSSKDPSPAPAPANRLANSTVNS 305
 5 VAFNFGPNRRVFKRVSNIHGRIDIFASKNFHLOKNTIGTRISLKLISGKIAS 63

RESULT 10
 ENTRY S55415 #type complete
 TITLE ATP-binding transport protein ywja - Bacillus subtilis
 ALTERNATE_NAMES ABC transporter (ATP-binding protein) ywja
 ORGANISM #formal_name Bacillus subtilis
 DATE 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999

ACCESSIONS S55415
 REFERENCE S55415
 #authors Glaser, P.; Danchin, A.
 #description submitted to the EMBL Data Library, May 1995
 #submission Cloning and sequencing of the Bacillus subtilis chromosomal region from 320 degrees to 321 degrees.
 #accession S55415

GENETICS #molecule-type DNA
 #residues 1-575 ##label GIA
 #cross-references EMBL:249782; NID:9853752; PIDN:CAA9862.1; PID:9853754

REFERENCE A69580
 #authors Kunst, F.; Ogasawara, N.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, M.G.; Besieres, P.; Bolotin, A.; Borchert, S.; Boriss, R.; Boutsier, L.; Brans, A.; Braun, M.; Brignell, S.C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, S.K.; Codani, U.J.; Connerton, I.F.; Cummings, N.J.; Daniel, R.A.; Denzot, F.; Devienne, K.M.; Duesterhoeft, A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Erington, J.; Fabret, C.; Ferrari, E.; Foulger, D.; Fitz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier, N.; Ghm, S.Y.; Glaser, P.; Goffeau, A.; Gollightly, E.J.; Grand, G.; Giuseppe, G.; Guy, B.J.; Haga, K.; Haelec, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Itaya, M.; Jones, L.; Joris, B.; Katamata, D.; Kasahara, Y.; Klaerr-Blanchard, M.; Klein, C.; Kobayashi, Y.; Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, S.; Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, C.; Medigue, C.; Medina, N.; Mellado, R.P.; Mizuno, M.; Moesli, D.; Nakai, S.; Noboka, M.; Noone, D.; O'Reilly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetlelle, D.; Potwolk, S.; Prescott, A.M.; Prescecan, E.; Puje, P.; Purnelle, B.; Rapoport, G.; Rey, M.; Reynolds, S.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadle, Y.; Sato, T.; Scanlon, E.; Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot, S.J.; Serro, P.; Shin, B.S.; Soldo, B.; Sorokin, A.; Tacconi, E.; Takagi, T.; Takahashi, T.; Takemura, K.; Takeuchi, M.; Tamakoshi, A.; Tanaka, S.; Terpestra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandenbol, M.; Vannier, F.; Vassart, A.; Viari, A.; Wandut, R.; Wedler, E.; Wedler, H.; Weitznegger, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

#journal Nature (1997) 390:249-256
 #title The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 #cross-references M0ID:98044033
 #accession G70059

Terstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, S.; Vandendol, M.; Vannier, F.; Vassart, A.; Vardi, A.; Wandutt, R.; Wedler, E.; Wedler, H.; Weltzner, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Yoshikawa, H.; Zimstein, E.; Yoshikawa, H.; Danchin, A.

#journal Nature (1997) 390:249-256
#title The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
#cross-references MIMD:98044033
#accession G69628
#status preliminary; nucleic acid sequence not shown; translation not shown

##molecule-type DNA
##residues 1-340 ##label KUN
##cross-references GB:299118; GB:AL009126; NID:g2635200; PIDN:CAB14862.1; PID:el184151; PID:g2635367
##experimental-source strain 168

GENETICS
#gene gapB
#classification glycolysis; NAD; oxidoreductase
#keywords
#feature 152,179
#summary #length 340 #molecular-weight 37476 #checksum 2288

Query Match
Best Local Similarity 38.9%; Pred. No. 2.08e+00;
Matches 21; Conservative 10; Mismatches 18; Indels 5; Gaps 5;

Db 1 MKVYVAFNGFGFGRKAMLDQIOYVAIINSSYSEIHLIKYDTI-HGR 53
1 MKVYVAFNGFGFGRKAMLDQIOYVAIINSSYSEIHLIKYDTI-HGR 50

RESULT 14
ENTRY S75065 #type complete
TITLE sensory transduction histidine kinase sll1590 - *Synechocystis* sp. (strain PCC 6803)
ALTERNATE_NAMES #formal_name *Synechocystis* sp.
ORGANISM PCC 6803
#variety 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Aug-1998

ACCESSIONS S75065
REFERENCE S74322
#authors Kaneo, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirose, M.; Sugita, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naro, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Mada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S.

#journal DNA Res. (1996) 3:109-136
#title Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.
#cross-references MIMD:97061201
#accession S75065
#status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 1-350 ##label KAN
##cross-references EMBL:D90910; GB:AB001339; NID:g1652956; PID:d1018660; PID:g1653010
##note the nucleotide sequence was submitted to the EMBL Data Library, June 1996

GENETICS
#start_codon GTG
#summary #length 350 #molecular-weight 39445 #checksum 2983

Query Match
Best Local Similarity 38.6%; Pred. No. 2.77e+00;
Matches 17; Conservative 12; Mismatches 11; Indels 4; Gaps 2;

Db 246 QVFNNTITAINHSPRGKVEISLTKNNHFOVLYDEGRCP 289
14 RRVEIKRVSNIH--GRRDI-FASKNFHLOKNTIGTGRIS 53

RESULT 15
ENTRY S61986 #type complete
TITLE subtilisin-like proteinase (EC 3.4.21.-) YSP3 precursor - yeast (*Saccharomyces cerevisiae*)
ALTERNATE_NAMES protein O2517; protein UNC478; protein YOR003w;
ORGANISM subtilisin-like proteinase III
#formal_name *Saccharomyces cerevisiae*
DATE 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

ACCESSIONS S61986
REFERENCE S61981
#authors Sterky, F.; Uhlen, M.
#summary submitted to the EMBL Data Library, December 1995
#accession S61986
##molecule-type DNA
##residues 1-478 ##label STM
##cross-references EMBL:U43491; NID:g1150992; PIDN:AAC49482.1; PID:g1150998

REFERENCE S6682
#authors Pettersson, B.; Sterky, F.; Uhlen, M.
#summary submitted to the Protein Sequence Database, July 1996
#accession S6688
##molecule-type DNA
##residues 1-478 ##label PRT
##cross-references EMBL:Z74911; NID:g1420091; PIDN:CAA99191.1; PID:e252316; PID:g1420092; MIPS:YOR003w

##experimental-source strain S288C

REFERENCE S72130
#authors Sterky, F.; Holmberg, A.; Pettersson, B.; Uhlen, M.
#summary The sequence of a 30 kb fragment on the left arm of chromosome XV from *Saccharomyces cerevisiae* reveals 15 open reading frames, five of which correspond to previously identified genes.
#cross-references MIMD:97051599
#accession S72135
##status nucleic acid sequence not shown; translation not shown
##molecule-type DNA
##residues 1-478 ##label STM
##cross-references EMBL:U43491; NID:g1150992; PIDN:AAC49482.1; PID:g1150998
##note the nucleotide sequence was submitted to the EMBL Data Library, December 1995

GENETICS
#gene SGD:YSP3
#cross-references SGD:S0005529; MIPS:YOR003w
#map_position 15R
#classification #superfamily subtilisin; subtilisin homology
#keywords hydrolase; serine proteinase
#feature 21-478
#domain signal sequence #status predicted #label SIG
#product subtilisin-like proteinase YSP3 #status predicted #label MART
#domain subtilisin homology #label SRT
#active_site Asp, His, Ser #status predicted
#length 478 #molecular-weight 52089 #checksum 1502

SUMMARY #length 478 #molecular-weight 52089 #checksum 1502

Query Match
Best Local Similarity 30.2%; Pred. No. 3.70e+00;
Matches 13; Conservative 15; Mismatches 13; Indels 2; Gaps 2;

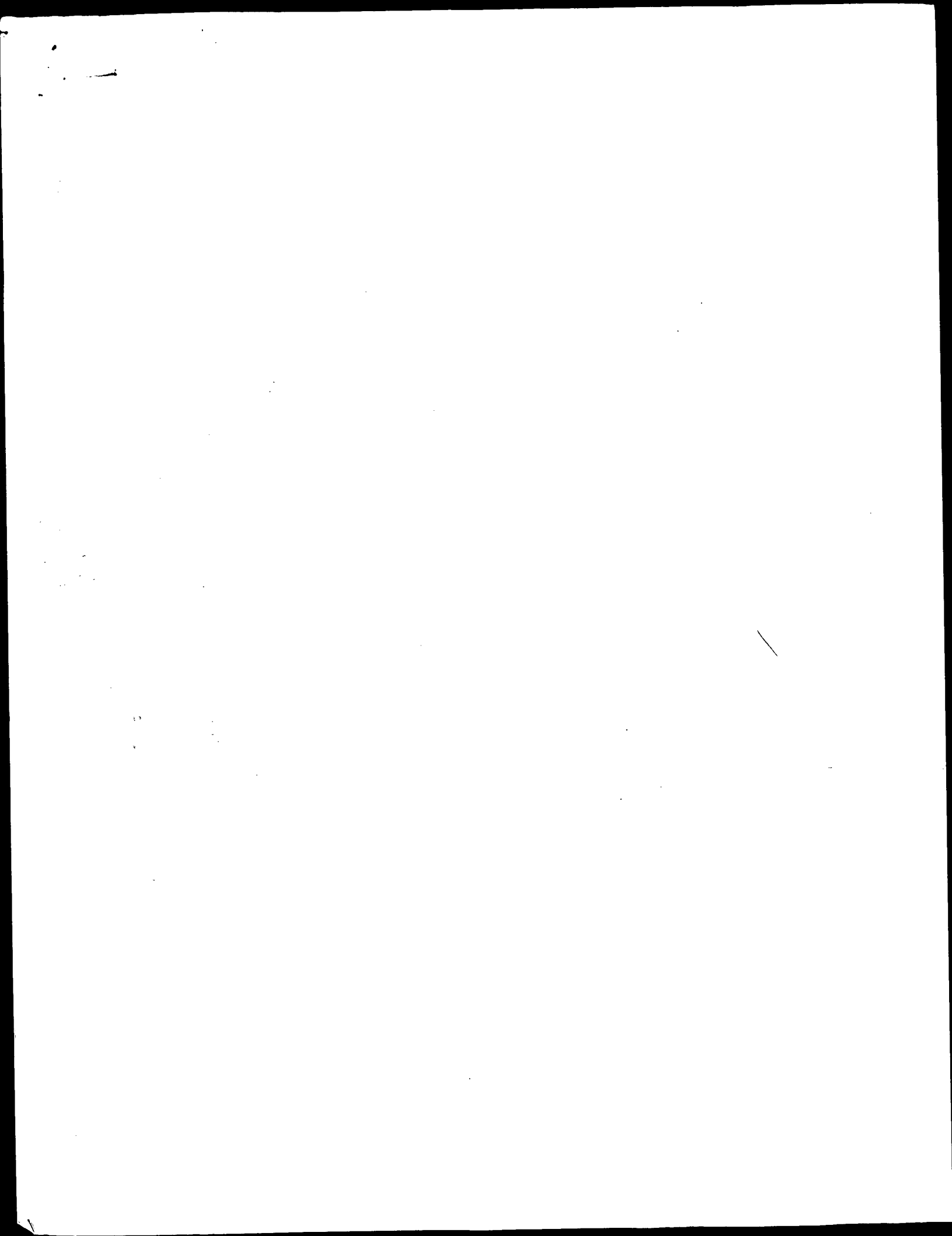
Db 380 VDVFP-GLINMSTYIGS-RNATLSLSTGSMASPHVAGILSYF 420
31 IDIFASKNFHLOKNTIGTGRISLTKSKIASRVDGIIAAV 73

Search completed: Mon Jun 19 15:53:58 2000

Wed Jun 21 09:22:48 2000

Job time : 14 secs.

US-09-142-524A-1.rpr



(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Mon Jun 19 15:52:40 2000; Mspar time 5.85 Seconds
Tabular output not generated. 416,406 Million cell updates/sec

Title: >US-09-142-524A-1
Description: (1-80) from US09142524A.pep
Perfect Score: 569
Sequence: 1 MKYTVAFNCFGNRRVFIRK.....IASRVYDGIITAYQNPASWK 80

Scoring table:
Gap 11
PAM 150

Searched: 83857 seqs, 30454973 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot38
1:swissprot

Statistics: Mean 40.706; Variance 73.263; scale 0.556

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	129	22.7	514	1	MPA2_CRYTA POSSIBLE POLYGACTACTRO	3.32e-07
2	98	17.2	633	1	TOP1_THEMA DNA TOPOISOMERASE I (E	3.02e-02
3	97	17.0	862	1	FKH2_YEAST FORK HEAD PROTEIN HOMO	4.25e-02
4	96	16.9	507	1	DNA_RHIME CHROMOSOMAL REPLICATIO	5.96e-02
5	95	16.7	110	1	Y12K_SMSV4 POSSIBLE 12 KD NUCLEIC	8.34e-02
6	95	16.7	374	1	SBP_CRYTA SUGI BASIC PROTEIN PRE	8.34e-02
7	95	16.7	680	1	KALM_HUMAN KALLIMANN SYNDROME PROT	8.34e-02
8	94	16.5	575	1	YWJA_BACSU GLYCERALDEHYDE ABC TRANS	1.16e-01
9	89	15.6	340	1	G3P2_BACSU GLYCERALDEHYDE 3-PROSP	5.96e-01
10	87	15.3	478	1	YSP3_YEAST SUBTILISIN-LIKE PROTEA	1.13e+00
11	86	15.3	629	1	FRE7_YEAST FERRIC REDUCTASE TRANS	1.13e+00
12	86	15.1	532	1	PPCK_AMASU PHOSPHOENOLPYRUVATE CA	1.54e+00
13	86	15.1	1070	1	YQFA_YEAST HYPOHETICAL 123.0 KD	1.54e+00
14	85	14.9	331	1	YQ51_YEAST HYPOHETICAL 35.6 KD P	2.10e+00
15	85	14.9	394	1	DNA_YEAST CHROMOSOMAL REPLICATIO	2.10e+00
16	84	14.8	263	1	DNA_YEAST CHROMOSOMAL REPLICATIO	2.10e+00
17	83	14.6	302	1	ATCR_HUMAN CALCIDIOL-TRANSPORTING A	3.89e+00
18	83	14.6	1205	1	HYPOHETICAL 44.4 KD P	3.89e+00
19	83	14.6	1745	1	HYPOHETICAL 44.4 KD P	3.89e+00
20	82	14.4	249	1	Y084_METJA HYPOHETICAL ARP-BINDI	5.27e+00
21	82	14.4	389	1	PKNS_MYCPN PUTATIVE SERINE/THREON	5.27e+00
22	81	14.2	1011	1	SECA_PEA PREPROTEIN TRANSLOCASE	7.11e+00
23	80	14.1	155	1	RS7_MYCCE 30S RIBOSOMAL PROTEIN	9.57e+00

24	80	14.1	159	1	RK35_SPIOL 50S RIBOSOMAL PROTEIN	9.57e+00
25	80	14.1	274	1	Y179_MYCCE HYPOHETICAL ABC TRANS	9.57e+00
26	80	14.1	311	1	NFE2_RHIME NFE2 PROTEIN.	9.57e+00
27	80	14.1	317	1	YM91_YEAST HYPOHETICAL 35.9 KD P	9.57e+00
28	80	14.1	383	1	METL_YEAST S-ADENOSYLMETHIONINE S	9.57e+00
29	80	14.1	419	1	WM01_YEAST PROTEIN M.	9.57e+00
30	80	14.1	421	1	WM01_VACCV PROTEIN M.	9.57e+00
31	80	14.1	472	1	WM01_VACCV PROTEIN M.	9.57e+00
32	80	14.1	493	1	GLYM_CANAL SERINE HYDROXYMETHYLTR	9.57e+00
33	80	14.1	719	1	PRH1_SCHPO PROBABLE ATP-DEPENDENT	9.57e+00
34	79	13.9	177	1	PBAS_RAT PROBASIN PRECURSOR (PB	1.28e+01
35	79	13.9	243	1	RS4E_PYRO 30S RIBOSOMAL PROTEIN	1.28e+01
36	79	13.9	325	1	ARGB_BACSU ACETYLGLUTAMATE KINASE	1.28e+01
37	79	13.9	325	1	ARGB_BACSU BASIC MEMBRANE PROTEIN	1.28e+01
38	79	13.9	436	1	DXR_MYCVU 1-DEOXY-D-XYLULOSE 5-P	1.28e+01
39	79	13.9	523	1	C9B1_GLYEC CYCLOCHROME P450 93B1 (1.28e+01
40	79	13.9	719	1	AAS_ECOLI AAS BIFUNCTIONAL PROTE	1.28e+01
41	79	13.9	1010	1	YK01_CARBL HYPOHETICAL 113.2 KD	1.28e+01
42	79	13.9	1103	1	CYGF_BOVIN RETINAL GUANYLYL CYCLA	1.28e+01
43	78	13.7	176	1	YCE7_DROME HYPOHETICAL 18.8 KD P	1.72e+01
44	78	13.7	473	1	ATPB_BACCA ATP SYNTHASE BETA CHAI	1.72e+01
45	78	13.7	577	1	YTFW_ECOLI HYPOHETICAL 64.8 KD P	1.72e+01

ALIGNMENTS

RESULT	1	STANDARD	PRT	514 AA.
ID	MPA2_CRYTA			
AC	P43212;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, last sequence update)			
DT	01-NOV-1997 (Rel. 35, last annotation update)			
DE	POSSIBLE POLYGACTACTROSE PRECURSOR (EC 3.2.1.15) (PG) (PECTINASE)			
DE	(MAJOR POLLEN ALLERGEN CRY 2) (CRY 2 II).			
OS	Cryptomeria japonica (Japanese cedar).			
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;			
OC	euphyllophytes; Streptophyta; Coniferophyta; Coniferales;			
OC	Taxodiaceae; Cryptomeria.			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUE-POLLEN;			
RC	MEDLINE; 95010777.			
RA	Namda M., Kurose M., Torioge K., Hino K., Taniguchi Y., Fukuda S.,			
RA	Usui M., Kurimoto M.,			
RT	"Molecular cloning of the second major allergen, Cry 2 II, from			
RT	Japanese cedar pollen."			
RL	FEBS Lett. 353:124-128(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE-POLLEN;			
RC	MEDLINE; 94271186.			
RA	Komiyama N., Sone T., Shimizu K., Morikubo K., Kino K.,			
RA	"cDNA cloning and expression of Cry 2 II the second major allergen of			
RT	Japanese cedar pollen."			
RL	Biochem. Biophys. Res. Commun. 201:1021-1028(1994).			
RN	[3]			
RP	SEQUENCE OF 55-64.			
RC	MEDLINE; 90342988.			
RA	Sakaguchi M., Inouye S., Tanai M., Ando S., Usui M., Matunasi T.,			
RT	"Identification of the second major allergen of Japanese cedar			
RL	pollen."			
RL	Allergy 45:309-312(1990).			
CC	-1- CATALYTIC ACTIVITY: RANDOM HYDROLYSIS OF 1,4-ALPHA-D-			
CC	GALACTOSIDURONIC LINKAGES IN PECTATE AND OTHER GALACTURONANS.			
CC	-1- SUBCELLULAR LOCATION: SECRETED OR AMYLOPLAST (POTENTIAL).			
CC	-1- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES			
CC	(POLYALACTONASES).			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			

entitles requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: D3765; BAA07021.1; -

CC EMBL: D29772; BAA06172.1; -

DR PROSITE: PS00502; POLYGALACTURONASE; 1.

DR PFM: PFO0295; Glyco_hydro.28; 1.

KM Hydrolase; Glycosidase; Cell wall; signal; zymogen; Fruit ripening;

KM Amyloplast; Glycoprotein; Allergen.

FT SIGNAL 1 2

FT PROPEP 45

FT CHAIN 46 433

FT ACT_SITE 434 514

FT CARBOHYD 278 278

FT CARBOHYD 460 460

FT CARBOHYD 472 472

FT CONFLICT 5 5

FT CONFLICT 12 12

FT CONFLICT 34 35

FT CONFLICT 37 37

FT CONFLICT 88 88

FT CONFLICT 98 98

FT CONFLICT 451 451

FT CONFLICT 454 454

FT CONFLICT 504 504

FT CONFLICT 507 507

SEQUENCE 514 AA; 56645 MW; 624611C3FAD6302 CRC64;

Query Match 22.7%; Score 129; DB 1; Length 514;

Best Local Similarity 100.0%; Pred. No. 3.32e-07;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 236 IDIFASKNFHLOKNTGTG 254

Y 31 IDIFASKNFHLOKNTGTG 49

RESULT 2 STANDARD; PRT; 633 AA.

ID TOP1-THEMA

AC P46799;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-FEB-2000 (Rel. 39, Last annotation update)

DE DNA TOPOISOMERASE I (EC 5.99.1.2) (OMEGA-PROTEIN) (RELAXING ENZYME)

DE (UNWISTING ENZYME) (SMIWELEASE).

GN TOPA OR TM0258.

OS Thermotoga maritima.

OC Bacteria; Thermotogales; Thermotoga.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-MSB8 / DSM 3109;

RA MEDLINE: 96136548.

RA Bouthier de la Tour C., Kaltoun H., Portemer C., Confalonieri F.,

RA Huber R., Duguet M.;

RT "Cloning and sequencing of the gene coding for topoisomerase I from

RT the extremely thermophilic eubacterium, Thermotoga maritima.";

RL Biochim. Biophys. Acta 1264:279-283(1995).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-MSB8 / DSM 3109;

RA MEDLINE: 99287316.

RA Nelson K.E., Clayton R.A., Gill S.R., Gwin M.L., Dodson R.J.,

RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

RA McDonald L., Utterback T.R., Pratt M.S., Phillips C.A., Richard D.,

RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richard D.,

RA Saldeberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

RT "Evidence for lateral gene transfer between Archaea and Bacteria from

RT genome sequence of Thermotoga maritima.";

RL Nature 399:323-329(1999).

CC -1- FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE

CC CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

CC -1- CATALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED

CC DNA, FOLLOWED BY PASSAGE AND REJOINING.

CC -1- SUBUNIT: MONOMER (BY SIMILARITY).

CC -1- MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA

CC BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, IN

CC WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOSPHORUS

CC AT ONE END OF THE ENZYME-SEVERED DNA STRAND.

CC -1- SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE

CC FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: U27841; AAA68949.1; -

DR EMBL: AE001708; AAD35346.1; -

DR TIGR: TM0258; -

DR HSSP: P06612; IECL.

DR PRINTS: PR00417; PRPISMRASEI.

DR PROSITE: PS00396; TOPOISOMERASE_L_PROK; 1.

DR PFM: PFO1131; Topoisom_dac; 1.

KW Isomerase; Topoisomerase; DNA-binding.

FT ACT_SITE 288 288

FT ACT_SITE 288 288

SEQUENCE 633 AA; 72694 MW; F7262A044060CFE9 CRC64;

Query Match 17.2%; Score 98; DB 1; Length 633;

Best Local Similarity 26.6%; Pred. No. 3.02e-07;

Matches 17; Conservative 18; Mismatches 26; Indels 3; Gaps 3;

DB 154 VLNR 157

Y 77 ASWK 80

RESULT 3 STANDARD; PRT; 862 AA.

ID FKX2-YEAST

AC P41813;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last annotation update)

DE FORK HEAD PROTEIN HOMOLOG 2.

DE FKX2 OR YNL068C OR NZ403 OR YNL2403C.

GN Saccharomyces cerevisiae (Baker's yeast).

OS Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;

OC Saccharomycetaceae; Saccharomyces.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-S288C;

RA Zhu G., Davis T.N.;

RT Submitted (XX-1995) to the EMBL/Genbank/DBJ databases.

RL [2]

RP SEQUENCE FROM N.A.

RC STRAIN-S288C / FY1679;

RA MEDLINE: 96267764.

RA Boehlmann R., Phillipsen P.;

RT "Sequencing a cosmid clone of Saccharomyces cerevisiae chromosome XIV

RT reveals 12 new open reading frames (ORFs) and an ancient duplication

RT of six ORFs.";

RL Yeast 12:391-402(1996).

RN [3]

RP SEQUENCE OF 1-440 FROM N.A.

RC STRAIN-S288C / FY1676;

RA MEDLINE: 96021608.

RA Berge P., Dolnon F., Crouzet M.;

RT "The sequence of a 44 420 bp fragment located on the left arm of

RT chromosome XIV from Saccharomyces cerevisiae.";


```

RL  Yeast 11:967-974(1995).
RN  [4]
RN  ERRATUM.
RX  MEDLINE: 97060022.
RA  Berger P., Doljono F., Crouzet M.:
RL  Yeast 12:297-297(1996).
CC  -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC  -1- SIMILARITY: CONTAINS 1 FORK-HEAD DOMAIN.
CC  -1- SIMILARITY: CONTAINS 1 FHA DOMAIN.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (see http://www.1b5-sib.ch/announce/
CC  or send an email to license@sib-sib.ch).
CC  -----
DR  EMBL: L38850; AAA60939.1; -
DR  EMBL: X86470; CAA60193.1; -
DR  EMBL: 271343; CAA95941.1; -
DR  EMBL: 271344; CAA95942.1; -
DR  EMBL: 012141; AAA99643.1; -
DR  SGD: L0002608; FKH2.
DR  PRINTS: PR00053; FORKHEAD.
DR  PROSITE: PS00657; FORK_HEAD_1; 1.
DR  PROSITE: PS00658; FORK_HEAD_2; 1.
DR  PROSITE: PS50006; FHA_DOMAIN; 1.
DR  PROSITE: PS50039; FORK_HEAD_3; 1.
DR  PFM: PF00250; Fork_head; 1.
DR  PFM: PF00498; FHA; 1.
KW  DNA-binding; Nuclear protein.
DR  DOMAIN 83 152 FHA.
FT  DNA_BIND 339 430 FORK-HEAD.
SQ  SEQUENCE 862 AA; 94374 MW; 68A03F5EB7BB5CP3 CRC64;

Query Match 17.0%; Score 97; DB 1; Length 862;
Best Local Similarity 26.7%; Pred. No. 4,25e-02;
Matches 20; Conservative 23; Mismatches 27; Indels 5; Gaps 5;

Db 65 AYAKLSGPNWYIYKDL-EVSI-GRNDPLNS-ALQNSDGVKNSYRVNIDLPKAVYSR 121
OY 6 AFNPG-GRNRVRFILKRVSNVILHGRRIDIFKSNFHLQKNTIGHGRRIISLKTSGIAAS 64
Db 122 K-HAIIRKYNINIGW 135
OY : || |::|
65 RVDGIATAYQNPM 79

RESULT 4
ID DNA_RHIME STANDARD; PRT; 507 AA.
AC P35890;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE CHROMOSOMAL REPLICATION INITIATOR PROTEIN DNA.
GN DNA.
OS Rhizobium meliloti.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinothizobium.
[1]
RP SEQUENCE FROM N.A.
RC STRAIN:1021.
RX MEDLINE: 95270610.
RA Margolin W., Bramhill D., Long S.R.;
RT "The dnaA gene of Rhizobium meliloti lies within an unusual gene
arrangement.";
RL J. Bacteriol. 177:2892-2900(1995).
-!- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE INITIATION AND REGULATION
OF CHROMOSOMAL REPLICATION. BINDS TO THE ORIGIN OF REPLICATION.
IT BINDS SPECIFICALLY DOUBLE-STRANDED DNA AT A 9 BP CONSENSUS
(DNAA BOX): 5'-TTATC(C/A)A(C/A)-A-3'. DNAA BINDS TO ATP AND TO
ACIDIC PHOSPHOLIPIDS.

```

```
CC -1- SIMILARITY: BELONGS TO THE DNAA FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as their content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
DR EMBL; L25439; AAA6258.1; -
DR EMBL; L39265; AAA91097.1; -
DR PRINTS; PRO0051; DNAA.
DR PROSITE; PS01008; DNAA; 1.
DR PFAM; PF00308; Dac_dnaA; 1.
KM DNA replication; DNA-binding; ATP-binding.
FT NP_BIND 208 215 ATP (PROBABLE).
SQ SEQUENCE 507 AA; 56531 MW; 76015F49184FCFA CRC64;

Query Match 16.9%; Score 96; DB 1; Length 507;
Best Local Similarity 24.3%; Pred. No. 5,96e-02;
Matches 17; Conservative 25; Mismatches 25; Indels 3; Gaps 3;

Db 422 VVAKHVNSQELVSNRRTYVKPPQIAMYSKTTT-PRSPPEIGRRGGDHDTVLHA 480
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
5 VAANQSGPNRVRFI-KRVSNVIIGHRIDIFASKNFHLQKNITGTRISLK-LTSGKA 62
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Db 481 VKRIEETISA 490
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 63 SRKVDGIIN 72

RESULT 5 STANDARD: PRT; 110 AA.
ID Y12K-SMSV4
AC P36289;
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 37, Last annotation update)
DE 15-DEC-1998 (Rel. 37, Last annotation update)
DS POSSIBLE 12 KD NUCLEIC ACID-BINDING PROTEIN.
OS San Miguel sea lion virus (serotype 4) (SMSV 4).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Calicivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX RA MEDLINE: 92410750.
RL Neill J.D.;
RT "Nucleotide sequence of the capsid protein gene of two serotypes of
RT San Miguel sea lion virus: identification of conserved and non-
RT conserved amino acid sequences among calicivirus capsid proteins.";
RL Virus Res. 24:211-222(1992).
CC -1- SIMILARITY: TO FELINE CALICIVIRUS 12 KD PROTEIN.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as their content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
DR EMBL; M87482; AAA16221.1; -
DR PIR; D48562; D48562.
SQ SEQUENCE 110 AA; 12566 MW; 14255D593827418E CRC64;

Query Match 16.7%; Score 95; DB 1; Length 110;
Best Local Similarity 28.9%; Pred. No. 8.34e-02;
Matches 13; Conservative 17; Mismatches 13; Indels 2; Gaps 2;

Db 10 FLNVYANAAYEGKKLDI-ASKGLQLSRALDTERAFNYDLAFEK 53
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
17 FIKRVSNVNIIGHRIDIFASKNFHLQKNITGTRISLK-LTSGSK 60
```

RESULT 6
ID SBP CRYJA STANDARD: PRT: 374 AA.
AC P16632:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE SUGI BASIC PROTEIN PRECURSOR (SBP) (MAJOR ALLERGEN CRY J 1) (CRY J 1).
OS Cryptomeria japonica (Japanese cedar).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Taxodiaceae; Cryptomeria.
PP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE-POLLEN:
RX MEDLINE: 94183234.
RA Sone T., Komiya N., Shimizu K., Kusakabe T., Morikubo K., Kino K.:
RT "Cloning and sequencing of cDNA coding for Cry j I, a major allergen of Japanese cedar pollen."
RL Biochem. Biophys. Res. Commun. 199:619-625(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-POLLEN:
RX Namba M., Kurose M., Torigoe K., Fukuda S., Kurimoto M.; Submitted (JUL-1994) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE OF 22-41.
RC TISSUE-POLLEN:
RX MEDLINE: 89031257.
RA Tanai M., Ando S., Usui M., Kurimoto M., Sakaguchi M., Inouye S., Matsubashi T.:
RT "N-terminal amino acid sequence of a major allergen of Japanese cedar pollen (Cry j I)."
RL FEBS Lett. 239:329-332(1988).
RN [4]
RP CARBOHYDRATES.
RX MEDLINE: 95003748.
RA Hijioka A., Matsumoto I., Kojima K., Ogawa H.;
RT "Antigenicity of the oligosaccharide moiety of the Japanese cedar (Cryptomeria japonica) pollen allergen, Cry j I."
RL Int. Arch. Allergy Immunol. 105:198-202(1994).
CC -1- PTM: CONTAINS FUCOSE/XULOSE-CONTAINING N-LINKED OLIGOSACCHARIDES.
CC -1- DISEASE: THIS PROTEIN IS THE MAJOR ALLERGEN OF JAPANESE CEDAR POLLEN, THE MOST COMMON POLLEN ALLERGEN IN JAPAN.
CC -1- MISCELLANEOUS: THE SEQUENCE OF CRY J I FORM A IS SHOWN HERE. FORM B DIFFERS IN SIX POSITIONS.
CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1. AMB A I/AMB A II/CRY J I SUBFAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D26544; BAA05442.1; -
DR EMBL: D26545; BAA05443.1; -
DR EMBL: D34639; BAA07020.1; -
DR PIR: A44773; A44773.
DR PFAM: PF00544; pec_lyase; 1.
DR PRINTS: PRO0807; AMBALERGEN.
KW Allergen; Glycoprotein; Multigene family; Signal.
FT SIGNAL 1 21
FT CHAIN 1 2
FT VARIANT 12 374 SUGI BASIC PROTEIN.
FT VARIANT 12 12 L -> F (IN CRY J 1-B).
FT VARIANT 143 143 H -> Y (IN CRY J 1-B).
FT VARIANT 202 202 S -> T (IN CRY J 1-B).
FT VARIANT 221 221 L -> S (IN CRY J 1-B).
FT VARIANT 358 358 Q -> H (IN CRY J 1-B).
FT VARIANT 361 361 K -> Q (IN CRY J 1-B).
FT CARBOHYD 158 158 POTENTIAL.

FT CARBOHYD 191 191 POTENTIAL.
FT CARBOHYD 293 293 POTENTIAL.
SQ SEQUENCE 374 AA; 40645 MW; 74AB25950248F56F CRC64;
Query Match 16.7%; Score 95; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 8.34e-02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB 234 MKYVAFNPGPN 246
1 MKYVAFNPGPN 13
RESULT 7
ID KALM HUMAN STANDARD: PRT: 680 AA.
AC P23352:
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE KALLMANN SYNDROME PROTEIN PRECURSOR (ADHESION MOLECULE-LIKE X-LINKED).
GN KALI OR KAL OR ADMIX OR KALIG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92005720.
RA Legouis R., Hardelin J.-P., Levilliers J., Claverie J.-M., Compain S., Wunderle V., Millaesau P., le Paslier D., Cohen D., Caterina D., Bougueleret L., Delamarre-Van de Wal H., Lutfalla G., Weissensbach J., Petit C.:
RT "The candidate gene for the x-linked Kallmann syndrome encodes a protein related to adhesion molecules."
RL Cell 67:423-435(1991).
RN [2]
RP REVISIONS.
RX MEDLINE: 93265164.
RA del Castillo I., Cohen-Salmon M., Blanchard S., Lutfalla G., Petit C.;
RT "Structure of the x-linked Kallmann syndrome gene and its homologous pseudogene on the Y chromosome."
RL Nat. Genet. 2:305-310(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE: 92018217.
RA Franco B., Gaillet S., Pragliola A., Incerti B., Bardoni B., Tonlorenzi R., Carrozo R., Maestrini E., Pieretti M., Tallon-Miller P., Brown C.J., Willard H.F., Lawrence C., Persico N.G., Camerino G., Ballabio A.;
RT "A gene deleted in Kallmann's syndrome shares homology with neural cell adhesion and axonal path-finding molecules."
RL Nature 353:529-536(1991).
RN [4]
RP SEQUENCE OF 1-71 FROM N.A.
RX MEDLINE: 96069588.
RA Cohen-Salmon M., Tronche F., del Castillo I., Petit C.;
RT "Characterization of the promoter of the human KAL gene, responsible for the x-chromosome-linked Kallmann syndrome."
RL Gene 164:235-242(1995).
RN [5]
RP VARIANTS.
RX MEDLINE: 93278384.
RA Hardelin J.-P., Levilliers J., Blanchard S., Carel J.-C., Leuenegger M., Plinard-Berelleto J.-P., Boulox P., Petit C.;
RT "Heterogeneity in the mutations responsible for x chromosome-linked Kallmann syndrome."
RL Hum. Mol. Genet. 2:373-377(1993).
CC -1- FUNCTION: THIS PROTEIN MAY BE A SECRETED ADHESION-LIKE MOLECULE WITH ANTI-PROTEASE ACTIVITY.
CC -1- DISEASE: MUTATED OR PARTIALLY DELETED IN KALLMANN SYNDROME, A GENETIC DISORDER THAT ASSOCIATES HYPOGONADOTROPIC HYPOGONADISM AND ANOSMIA. IN THIS DISEASE, THE NORMAL EMBRYONIC MIGRATION OF GNRH-SYNTHESIZING NEURONS FROM THE OLFACTORY PLACODES TO THE

HYPOTHALAMIC REGION AS WELL AS THE AXONAL EXTENSION OF OLFACTORY
NEURONS TOWARDS THE FOREBRAIN ARE IMPAIRED.
-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
-1- SIMILARITY: CONTAINS 1 MAP-TYPE 'FOUR-DISULFIDE CORE' DOMAIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
CC or send an email to license@isb-sdb.ch).

DR EMBL: M97282; AAA59202.1; -
DR EMBL: S60085; AAB20108.1; ALT_SEQ.
DR EMBL: X60299; CAA42841.1; -
DR EMBL: X82034; CAA57554.1; -
DR PIR: A40351; A40351.
DR PIR: S17982; S17982.
DR MIM: 147950; -
DR MIM: 308700; -
DR PRINTS: PRO0003; 4DISULPHCORE.
DR PROSITE: PS00317; 4.DISULFIDE_CORE; 1.
DR PFAM: PF00041; fn3; 3.
DR PFAM: PF00095; wap; 1.
KW Cell adhesion; Glycoprotein; Serine protease inhibitor; Signal;
KW Polymorphism; Disease mutation.
FT SIGNAL 1 20
FT CHAIN 21 680
FT DOMAIN 21 120
FT DOMAIN 131 176
FT DOMAIN 181 285
FT DOMAIN 286 402
FT DOMAIN 403 540
FT DOMAIN 541 661
FT CARBOHYD 71 71
FT CARBOHYD 209 209
FT CARBOHYD 300 300
FT CARBOHYD 470 470
FT CARBOHYD 553 553
FT CARBOHYD 564 564
FT VARIANT 267 267
FT VARIANT 534 534
FT VARIANT 534 534
FT CONFLICT 70 71
FT CONFLICT 373 373
FT CONFLICT 540 540
SQ SEQUENCE 680 AA; 76066 MW; 5D6ACCF14B5F5F8 CRC64;
Query Match 16.7%; Score 95; DB 1; Length 680;
Best Local Similarity 27.1%; Pred. No. 8.34e-02; Indels 1; Gaps 1;
Matches 16; Conservative 19; Mismatches 23;
Db 248 VQLDIPSRK-YQFRVAANVHGRTAPSKFRSSKDPSPAPAPANRLANSTVNS 305
OY 5 VAFNQFNPNRVFLTKRVSNVLIHGRRIDIPASKNFHLQNTIGRISLTKSGKIAS 63
RESULT 8
ID YWJA.BACSU STANDARD; PRT; 575 AA.
AC PA5861;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HYPOTHEICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN ACDA 5' REGION.
GN YWJA.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-168;

RA Glaser P., de la Fuente V., Danchin A.;
RL Submitted (May-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
CC (ABC TRANSPORTERS). MSBA SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sdb.ch/announce/>
CC or send an email to license@isb-sdb.ch).

DR EMBL: Z49782; CAA89862.1; -
DR EMBL: Z99123; CAB15751.1; -
DR HSSP: P13569; INBD.
DR SUBTILIST: BG11306; YWJA.
DR PROSITE: PS00211; ABC_TRANSPORTER; 2.
DR PFAM: PF00005; ABC_tran; 1.
DR PFAM: PF00654; ABC_membrane; 1.
KW Hypothetical protein; ATP-binding; Transport; Transmembrane.
FT TRANSMEM 16 36
FT TRANSMEM 50 70
FT TRANSMEM 132 152
FT TRANSMEM 154 174
FT TRANSMEM 244 264
FT TRANSMEM 267 287
FT NP_BIND 366 373
SQ SEQUENCE 575 AA; 64562 MW; 0F331439E675C8F4 CRC64;
Query Match 16.5%; Score 94; DB 1; Length 575;
Best Local Similarity 29.2%; Pred. No. 1.16e-01;
Matches 19; Conservative 17; Mismatches 27; Indels 2; Gaps 2;
Db 176 KMTKAFLLNKIDGFSRVAENVNIGIRLVOAFGEAEKRFPAVNNRFRVT-KLSY 234
OY 1 MKVTAFNQFNPNRVFLTKRVSNVLIHGRRIDIPASKNFHLQNTIGR-RISLTKSG 59
Db 235 KIMAK 239
OY 60 KIASR 64
RESULT 9
ID G3P2.BACSU STANDARD; PRT; 340 AA.
AC O34425;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE 2 (EC 1.2.1.12) (GAPDH).
GN GAPD.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE: 98048467.
RA Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
RT "Sequencing and functional annotation of the Bacillus subtilis genes
RT in the 200 kb rtm-dnaB region."
RL Microbiology 143:3431-3441(1997).
CC -1- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE
CC + NAD(+) = 1,3-DIPHOSPHATEGLYCERATE + NADH.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
CC DEHYDROGENASE FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

FT	ACT_SITE	245	245	CHARGE RELAY SYSTEM (BY SIMILARITY).
FT	ACT_SITE	407	407	
FT	CONFLICT	22	22	D -> E (IN REF. 1).
FT	CONFLICT	105	105	N -> D (IN REF. 1).
FT	CONFLICT	189	205	MISSING (IN REF. 1).
FT	CONFLICT	289	289	Y -> L (IN REF. 1).
SO	SEQUENCE	478 AA;	52089 MW;	3EAB11360235C6FF CRC64;
Query Match		15.3%;	Score 87;	DB 1; Length 478;
Best Local	Similarity	30.2%;	Pred. No. 1,13e+00;	
Matches	13; Conservative	15;	Mismatches 13;	Indels 2; Gaps 2;
Db	380	VDVFAP-GINIMSTYIGS-RNATLSGTSMA5PHAGILSYF	420	
Oy	31	IDIFASKNFHLQKNTIGTGRIKSLTSGIKASRRVDGIINAY	73	
RESULT	11	STANDARD;	PRT;	629 AA.
ID	FRET_YEAST			
AC	Q12333;			
DT	15-DEC-1998 (Rel. 37, Created)			
DT	15-DEC-1998 (Rel. 37, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	PERRIC REDUCTASE TRANSMEMBRANE COMPONENT 7 PRECURSOR.			
GN	FRET OR YOL152W.			
OS	Saccharomyces cerevisiae (Baker's yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;			
OC	Saccharomycetaceae; Saccharomyces.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-S288C / FY1679;			
RA	MEDLINE; 96132030.			
RA	Casamayor A., Aldea M., Casas C., Herrero E., Gamo F.J.,			
RA	Laitene M.J., Gancedo C., Arino J.,			
RT	"DNA sequence analysis of a 13 kbp fragment of the left arm of yeast			
RT	chromosome XV containing seven new open reading frames."			
RL	Yeast 11:1281-1288(1995).			
CC	-1- COFACTOR: FAD (PROBABLE).			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).			
CC	-1- SIMILARITY: BELONGS TO THE FRET / CYBB FAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on use			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; Z48239; CAA88276.1; -			
DR	EMBL; Z74894; CAA99174.1; -			
DR	SGD; L0003559; FRET7.			
KW	Electron transport; Transmembrane; Iron transport; FAD; NAD;			
KW	Glycoprotein; Signal; Multigene family.			
FT	CHAIN	1	2	POTENTIAL.
FT	STGNL	?	629	PERRIC REDUCTASE TRANSMEMBRANE COMPONENT
FT	NE_BIND	369	375	FAD (POTENTIAL).
FT	TRANSMEM	46	66	POTENTIAL.
FT	TRANSMEM	108	128	POTENTIAL.
FT	TRANSMEM	168	188	POTENTIAL.
FT	TRANSMEM	195	215	POTENTIAL.
FT	TRANSMEM	238	258	POTENTIAL.
FT	TRANSMEM	266	286	POTENTIAL.
FT	TRANSMEM	293	313	POTENTIAL.
FT	TRANSMEM	422	442	POTENTIAL.
FT	CARBOHYD	330	330	POTENTIAL.
FT	CARBOHYD	541	541	POTENTIAL.
SO	SEQUENCE	629 AA;	71996 MW;	2384480B9289C16F CRC64;
Query Match		15.3%;	Score 87;	DB 1; Length 629;
Best Local	Similarity	23.3%;	Pred. No. 1,13e+00;	
Matches	7; Conservative	14;	Mismatches 9;	Indels 0; Gaps 0;

Db 350 YSPGHIFFRTIDKGIISNHPFIPSAKY 379
 OY 10 FGPNRRVFIKRVSNVITIGRIDIFASKNF 39

RESULT 12
 ID PECK_AMASU STANDARD: PRT: 532 AA.

DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE PHOSPHOENOLPYRUVATE CARBOXYKINASE (pckA) gene."
 GN pckA.
 OS Anaerobiospirillum succiniciproducens.
 OC Bacteria; Proteobacteria; gamma subdivision; Succinivibrionaceae;
 CC Anaerobiospirillum.

RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29305;
 RX MEDLINE: 97316436.
 RA Laivenieks M., Vielle C., Zeikus J.G.;
 RT Cloning, sequencing, and overexpression of the Anaerobiospirillum
 succiniciproducens phosphoenolpyruvate carboxykinase (pckA) gene."
 RL Appl. Environ. Microbiol. 63:2273-2280(1997).
 CC -1- CATALYTIC ACTIVITY: ATP + OXALOACETATE -> ADP + PHOSPHOENOLPYRUVATE
 + CO(2).
 CC -1- PATHWAY: RATE-LIMITING GLUCONEOGENIC ENZYME.
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOENOLPYRUVATE CARBOXYKINASE (ATP)
 FAMILY.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: U95960; AAC45394.1; -
 DR HSRP: P22259; IOEN.
 DR PROSITE: PS00532; PEPCK_ATP; 1.
 DR PFAM: PF01293; PEPCK_ATP; 1.
 KW Glucogeneogenesis; Lyase; Decarboxylase; ATP-binding.
 FT NP BIND 242
 SO SEQUENCE 532 AA; 58643 MW; 983ABC71930F9E44 CRC64;

Query Match 15.1%; Score 86; DB 1; Length 532;
 Best Local Similarity 34.1%; Pred. No. 1.54e+00;
 Matches 15; Conservative 12; Mismatches 16; Indels 1; Gaps 1;

Db 421 KREMSGAAYLVNTGNGTGKRIKTRIGITDAI-IDGSIDT 463
 OY 29 RAIDIFASKNFHLQKNTIGTRISLKLTSKISRVDGIITAA 72

RESULT 13
 ID YH4_YEAST STANDARD: PRT: 1070 AA.

AC P38850;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE HYPOTHETICAL 123.0 KD PROTEIN IN SP016-REC104 INTERGENIC REGION.
 GN YHRI54W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 CC Saccharomycetaceae; Saccharomyces.

RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX MEDLINE: 94378003.
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
 RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,

RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
 RA Latreille P., Louis E.J., Macri C., Mardis E., Meneses S., Mouser L.,
 RA Nham M., Rifkin L., Riles L., St. Peter H., Trevasis E., Vaughan K.,
 RA Vignati D., Wilcox L., Wohlman P., Waterston R., Wilson R.,
 RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
 RT VII."
 RT Science 265:2077-2082(1994).

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: U10397; AAB68978.1; -
 DR PIR: S46755; S46755.
 DR PFAM: PF00533; BRCT; 5.
 KW Hypothetical protein.
 SO SEQUENCE 1070 AA; 123017 MW; 767931285BB52580 CRC64;

Query Match 15.1%; Score 86; DB 1; Length 1070;
 Best Local Similarity 31.5%; Pred. No. 1.54e+00;
 Matches 17; Conservative 15; Mismatches 20; Indels 2; Gaps 2;

Db 380 LTVATNFGSGRFYIOLIVE-IIGSLSTPEKTNHLTKSTGKRVYAK 432
 OY 3 VTVAFNQGPFRVFIKRVSNVITIGRIDIFASKNFHL-QKNTIGTRISL 55

RESULT 14
 ID YQFA_BACSU STANDARD: PRT: 331 AA.

AC P54466;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE HYPOTHETICAL 35.6 KD PROTEIN IN RPSU-PHOH INTERGENIC REGION.
 GN YQFA.
 OS Bacillus subtilis.
 CC Bacteria; Firmicutes; Bacillus/Clostridium group;
 CC Bacillus/Staphylococcus group; Bacillus.

RP SEQUENCE FROM N.A.
 RC STRAIN=168 / JH642;
 RA Kobayashi Y., Mizuno M., Masuda S., Takemaru K., Hosono S.,
 RA Sato T., Takeuchi M.;
 RL Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.

 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL: D84432; BA12473.1; -
 DR EMBL: Z99117; CAB14480.1; -
 DR SUBTILIST; BG11651; YQFA.
 KW Hypothetical protein; Transmembrane.
 FT TRANSMEM 6
 FT TRANSMEM 26
 FT TRANSMEM 48
 SO SEQUENCE 331 AA; 35641 MW; 484AD959F8109A7A CRC64;

Query Match 14.9%; Score 85; DB 1; Length 331;
 Best Local Similarity 22.8%; Pred. No. 2.10e+00;
 Matches 18; Conservative 29; Mismatches 26; Indels 6; Gaps 6;

Db 39 VKIST-FTLVGRRLKRVLPNRYVPLIAHAKAGLVNQTN-QLESHYLAGN-YD-RVVA 94
 OY 1 MKVIAFNQGPFRVFIKRVSNVITIGRIDIFASKNFHLQKNTIGTRISL 59

Release 3.1A John F. Collins, Biocomputing Research Unit
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Title:	>US-09-142-524A-1
Description:	(1-80) from US09142524A.pcp
Perfect Score:	569
Sequence:	1 MKVTVAFNQFGPNRRVFIKR.....

Searched: 225878 seqs, 69334122 residues

Database:

1:sp-archaea 2:sp-bacteria 3:sp-fungi 4:sp-human
5:sp-invertebrate 6:sp-mammal 7:sp-mhc 8:sp-organelle
9:sp-phage 10:sp-plant 11:sp-rodent 12:sp-unclassified
13:sp-vertebrate 14:sp-virus

Statistics: Mean 39.247; Variance 71.415; scale 0.550

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No
1	97	17.0	375	10	Q96385	CHAOL PRECURSOR.	6.15e+00
2	95	16.7	173	5	Q18291	D2058.2 PROTEIN.	1.22e+01
3	95	16.7	367	10	Q92M07	POLLEN MAJOR ALLERGEN	1.22e+00
4	94	16.5	893	5	Q02099	CODED FOR BY C. ELECAN	1.71e+00
5	91	16.0	1160	5	Q27829	PLASMA MEMBRANE CALCIU	4.65e+01
6	89	15.6	190	2	Q9X2E7	RIBOFLAVIN SYNTHASE, A	8.96e+01
7	88	15.5	108	14	Q09783	CAPSID.	1.24e+00
8	88	15.5	350	2	P73865	SENSORY TRANSDUCTION H	1.24e+00
9	87	15.3	110	14	P68682	CAPSID PROTEIN.	1.71e+00
10	87	15.3	394	10	P85457	PEPCATE LASE LIKE PRO	1.71e+00
11	87	15.3	394	10	Q04456	PEPCATE LASE LIKE PRO	1.71e+00
12	87	15.3	478	5	Q04153	Q4969.3 PROTEIN.	1.71e+00
13	86	15.1	440	2	Q06961	HYPOHETICAL 47.7 KD P	2.36e+00
14	86	15.1	586	5	Q17813	HYPOHETICAL 47.7 KD P	2.36e+00
15	86	15.1	802	10	Q38802	CO8B6.1 PROTEIN.	2.36e+00
16	85	14.9	84	14	Q08973	ENT-KAURENE SYNTHASE	3.24e+00
17	85	14.9	790	8	Q02718	ORF 1, ORF 2 AND ORF 3	3.24e+00
18	84	14.8	270	2	P73013	90.8 KD REVERSE TRANSC	4.43e+00
19	84	14.8	360	2	Q92G19	HYPOHETICAL 30.0 KD P	4.43e+00
20	84	14.8	647	3	Q92445	HYPOHETICAL 41.5 KD P	4.43e+00
						PUTATIVE MITOCHONDRIAL	4.43e+00

21	84	14.8	1330	2	053689	HYPOTHETICAL 145.2 KD	4.43e+00
22	84	14.8	3229	5	026912	PROTEIN 1 OF A DISPERS	4.43e+00
23	83	14.6	288	2	050267	MOAR.	6.05e+00
24	83	14.6	773	10	080631	FILB6.10 PROTEIN.	6.05e+00
25	83	14.6	1170	4	018617	PLASMA MEMBRANE CALCIT	6.05e+00
26	83	14.6	1259	14	039KCS	STRUCTURAL POLYPEPTIDE	6.05e+00
27	83	14.6	1873	14	083044	METHYLTRANSFERASE.	6.05e+00
28	83	14.6	2272	5	017329	GAG, POL. AND ENV PROTE	6.05e+00
29	82	14.4	289	5	001613	COSMID T3.9H12.	8.25e+00
30	82	14.4	325	6	028875	BAND 6 POLYPEPTIDE B6P	8.25e+00
31	82	14.4	390	10	065388	F1F1.22 PROTEIN.	8.25e+00
32	82	14.4	454	3	078879	FUSION YEAST (FRAGEN	8.25e+00
33	82	14.4	497	2	092D05	HISTIDINE KINASE SENS	8.25e+00
34	82	14.4	533	5	001617	HYPOTHETICAL 60.7 KD P	8.25e+00
35	82	14.4	534	5	018636	ZC443.6 PROTEIN.	8.25e+00
36	82	14.4	725	4	013835	BAND 6-PROTEIN.	8.25e+00
37	82	14.4	726	4	015132	PLAKOPHILIN.	8.25e+00
38	82	14.4	727	6	028161	PLAKOPHILIN.	8.25e+00
39	82	14.4	1195	2	006459	ALPHA SUBUNIT OF NITRA	8.25e+00
40	81	14.2	232	1	093779	ASPARTATE RACEMASE.	1.13e+01
41	81	14.2	402	12	09WTF5	TRANSPOSASE OF TND10.	1.13e+01
42	81	14.2	534	5	001614	HYPOTHETICAL 60.9 KD P	1.13e+01
43	81	14.2	728	11	P97350	PLAKOPHILIN 1.	1.13e+01
44	81	14.2	982	5	009532	HYPOTHETICAL 110.9 KD	1.13e+01
45	81	14.2	1116	5	015725	LIR-BETROTRANSPONSON SK	1.13e+01

ALIGNMENTS

RESULT	1
ID	Q96385
AC	006385.
	PRELIMINARY;
	PRT;
	375 AA

[illegible]

GN D2085.2. PROTEIN.
 CC Caenorhabditis elegans.
 CC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
 CC Rhabditina; Rhabditoidea; Rhabditidae; Pelodierinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BAYNES C.;
 RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RP MEDLIN; 94150718.
 RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BOWFIELD J., BURTON J., CONNELL M., COSEY T., COOPER J., COTLSON A.,
 RA CRAWTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAKINS T., KIRSTEN T., LAISTER N., LARRELL P.,
 RA JONES M., KESHAM J., KIRSTEN T., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA LIGHTNING J., LOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFEEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULTON J.,
 RA THIERRI-MIEG J., THOMAS K., VAUGHN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLIDAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 DR EMBL; 254284; CAA91060.1;
 SQ SEQUENCE 173 AA; 20523 MW; 6884DF8F CRC32;

[illegible]

```

RESULT 3
ID Q9ZNU7 PRELIMINARY: PRT; 367 AA.
AC Q9ZNU7;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE POLLEN MAJOR ALLERGEN 1-2.
OS Juniperus ashei (Ozark white cedar).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales;
OC Taxodiaceae; Juniperus.
[1]
RP SEQUENCE FROM N.A.
RA MIDONO-HORUTTI T.M., GOLDBLUM R.M., KUROSKY A., WOOD T.G.,
RA BROOKS E.G.;
RT "Molecular Cloning of mountain cedar (Juniperus ashei) pollen major
RT allergen, jun a.1.";
RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF106663; RAD03609.1; -.
DR EMBL: AF106662; RAD03608.1; -.
DR EMBL: 36544; Junas:1088;36544.
DR MENDEL, 36545; Junas:1088;36545.
DR MENDEL, 367 AA; 39824 MW; 4C2DB630 CRC32;
SQ SEQUENCE

```

Query Match	16.7%	Score 95;	DB 10;	Length 367;
Best Local Similarity	100.0%;	Pred. No. 1.22e-01;		
Matches	13; Conservative	0; Mismatches	0; Indels	0; Gaps

```

Db      234 MKVTVAFNQFGPN 246
        |||||
QY      1 MKVTVAFNQFGPN 13

```

RESULT	4	PRELIMINARY;	PRT;	893 AA.
ID	002099			
AC	002099;			
DT	01-JUN-1997 (TREMBLrel. 04, Created)			
DT	01-JUL-1997 (TREMBLrel. 04, Last sequence update)			
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)			
DE	CODED FOR BY C. ELEGANS CDNA YK23C8.3.			
GN	C18E3.3.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;			
OC	Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-BRISTOL N2;			
RX	MEDLINE; 94150718.			
RA	WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,			
RA	BONFIELD J., BURTON J., CONNELL M., COPESEY T., COOPER J., COULSON A.,			
RA	CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,			
RA	GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,			
RA	JONES M., KERSHAW J., KISTEN T., LAISTER N., LATRILLE P.,			
RA	LIGHTNING J., LOYD C., MCMURRAY A., MORIMORE B., O'CALLAGHAN M.,			
RA	PARSONS J., PERCY C., RIEKEN L., ROOPA A., SAUNDERS D., SHONKKEEN R.,			
RA	SMALDON N., SMITH A., SONNHAMMER E., STADEN R., STULSON J.,			
RA	THIERRE-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,			
RA	WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLMAN P.;			
RT	2.2 kb of contiguous nucleotide sequence from chromosome III of C.			

KI [elegans](#),
 RL [Nature](#) 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA CONNELL M., MAGGI L.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF000265; AAB52941.1; -
 SQ SEQUENCE 893 AA; 102424 MW; 696AF324 CRC32;

Query Match	16.5%	Score 94	DB 5	Length 893
Best Local Similarity	31.3%	Pred. No. 1.71e-01		
Matches	20	Conservative	20	Mismatches 20; Indels 4; Gaps 4
Db	602	VSUKANNVPERAP-FTWYSTRKNOLESLPEYTPARRISLOFRLKLTISNOKPD-IFKQY	659	
OY	16	VFKRNSNVIIHRRRIDFASKN-F-HLCKNTIGTGRISLTSGKTAASRRVDIIIMAY	73	
		:		
Db	660	HLPT	663	
OY	74	QNPRA	77	

```

ID      RESULT      5
Q27829 PRELIMINARY;   PRT;    1160 AA.
AC      Q27829;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE      PLASMA MEMBRANE CALCIUM ATPASE.
OS      Paraméciea tetraurelia.
OC      Eukaryota; Alveolata; Ciliophora; Nassophorea; Periculiida; Paramécium
[1]
RN      SEQUENCE FROM N.A.
RP
RC      STRAIN=515;
RA      ELWESS N.L., VAN HOUTEN J.L.;
RL      Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR      EMBL: U05880; AAB81284.1;
DR      PROSITE: PS00154; AFrase.F1_e2: 1.
DR      Pfam: PF00122; El_e2_ATPase: 2.
DR      PRINTS: P00119; CATTPASE.

```


KM Hydrolase; Transmembrane; Phosphorylation; ATP-binding.
 FT MOD_RES 442 442 PHOSPHORYLATION (PROBABLE).
 SQ SEQUENCE 1160 AA; 130984 MW; 68C09A2D CRC32;

Query Match 16.0%; Score 91; DB 5; Length 1160;
 Best Local Similarity 26.8%; Pred. No. 4,65e-01;
 Matches 15; Conservative 16; Mismatches 22; Indels 3; Gaps 3;

Db 543 MSVVDTHNGLPVRKLYKASSETIVOSLTHMHTYDDOKLKGVDIQEIERIS 598
 1 MKVTAFFNQFG-PNRKRVFKRVSNTIING-RRIDFASKNFHLQ-KNITIGRRIS 53

RESULT 6

ID Q9X2E7 PRELIMINARY; PRT; 190 AA.

AC Q9X2E7;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE RIPOFLAVIN SYNTHASE, ALPHA SUBUNIT.
 GN TM1827.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogales; Thermotoga.

RP SEQUENCE FROM N.A.
 RX MEDLINE: 99287316.

RA NELSON K.E., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,
 RA HART D.H., HICKLEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
 RA MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M.,
 RA STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
 RA HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,
 RA SMITH H.O., VENTER J.C., FRASER C.M.,
 RT "Evidence for lateral gene transfer between Archaea and bacteria from
 RT genome sequence of *Thermotoga maritima*.";
 RL Nature 393:323-329(1999).
 RN [1]

RP SEQUENCE FROM N.A.

RA NELSON K.E., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,
 RA HART D.H., HICKLEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
 RA MCDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M.,
 RA STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
 RA HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,
 RA SMITH H.O., VENTER J.C., FRASER C.M.,
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE001819; AAD36890.1; -
 SQ SEQUENCE 190 AA; 21678 MW; F999479B CRC32;

Query Match 15.6%; Score 89; DB 2; Length 190;
 Best Local Similarity 28.6%; Pred. No. 8,96e-01;
 Matches 10; Conservative 13; Mismatches 11; Indels 1; Gaps 1;

Db 60 RTNLFVSRFYNLEK-SIALGSRVHGHLVYGHWD 93
 29 RRIDFASKNFHLQKNITIGRRISLKTSGKTAS 63

RESULT 7

ID Q09783 PRELIMINARY; PRT; 108 AA.

AC Q09783;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE CAPSID.
 OS San Miguel sea lion virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Calicivirus.
 RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN-SMRY-17;
 RA MEDLINE: 98187296.
 RA WATSON D.O., BERKE T., DINTLOS M.B., POET S.E., ZHONG W.M., DAI X.M.,
 RA JIANG X., GOLDING B., SMITH A.W.,
 RT "Partial characterization of the genome of nine animal

RT caliciviruses.";
 RL Arch. Virol. 141:2443-2456(1996).
 DR EMBL: U52005; AAC57041.1; -
 SQ SEQUENCE 108 AA; 12354 MW; 476A3E95 CRC32;

Query Match 15.5%; Score 88; DB 14; Length 108;
 Best Local Similarity 35.3%; Pred. No. 1,24e+00;
 Matches 12; Conservative 12; Mismatches 9; Indels 1; Gaps 1;

Db 10 FLNGVANAALIEGKRLD-ASKGLQKRLALDTER 42
 17 FIKRVSNVHIGRRIDFASKNFHLQKNITIGRR 50

RESULT 8

ID P73865 PRELIMINARY; PRT; 350 AA.

AC P73865;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
 DE SENSOR TRANSDUCTION HISTIDINE KINASE.
 OS Synechocystis sp. (Strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-PCC6803;

RA TABATA S.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN-PCC6803;

RA KANEKO T., SANO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
 RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAKOTO S., KIMURA T.,
 RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
 RA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
 RA TABATA S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL: D90910; BA01927.1; -
 DR FRAM; PF00512; signal; 1.
 SQ SEQUENCE 350 AA; 39445 MW; EEF2A0B CRC32;

Query Match 15.5%; Score 88; DB 2; Length 350;
 Best Local Similarity 38.6%; Pred. No. 1,24e+00;
 Matches 17; Conservative 12; Mismatches 11; Indels 4; Gaps 2;

Db 246 QRVFNNTLTNAINSPRGKVEISLTSKNNHFOYQVDEGRGIP 289
 14 RRVFKRVSNTIIG-GRIDT-FASKNFHLQKNITIGRRIS 53

RESULT 9

ID P99682 PRELIMINARY; PRT; 110 AA.

AC P99682;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE CAPSID PROTEIN.
 OS vesicular exanthema of swine virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Calicivirus.
 RN [1]

RP SEQUENCE FROM N.A.

RA NEILL J.D., MEYER R.F., SEAL B.S.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U76874; AAC13890.1; -
 SQ SEQUENCE 110 AA; 12649 MW; 2998BA4B CRC32;

Query Match 15.3%; Score 87; DB 14; Length 110;

RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA BADCOCK K., CHURCHER C.M.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA BROSCHE R., PARKHILL J., BARRELL B.G., RAJANDREAN M.A.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37RV;
 RA MEDLINE: 96181548.
 RA PHILIPP W.J., POULET S., EIGMEIER K., PASCOPELLA L.,
 RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
 RA COLE S.T.;
 RT "An integrated map of the genome of the tubercle bacillus,
 RT Mycobacterium tuberculosis H37RV, and comparison with Mycobacterium
 RT leprae";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996).
 DR EMBL: AL022121; CAI8015.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 440 AA; 47687 MW; 608523P4 CRC32;

Query Match 15.1%; Score 86; DB 2; Length 440;
 Best Local Similarity 36.7%; Pred. No. 2.36e+00;
 Matches 11; Conservative 11; Mismatches 7; Indels 1; Gaps 1;
 DB 227 RRVYLDIGRMAAGRV-GVDTADPAGW 255
 11: - - - - - 11: - - - - - 11: - - - - -
 QY 50 RRLSLKTSKGIASRRVDCIILAIYQNPASW 79

RESULT 14
 AC 017813; PRELIMINARY; PRT; 586 AA.
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-MAY-1999 (TRENBLREL. 10, Last annotation update)
 DE C08B6.1 PROTEIN.
 GN C08B6.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditiia; Rhabditida;
 OC Rhabditiia; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA WILKINSON J.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BOUNFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
 RA CRAYTON M., DEAR S., DU Z., DUBREIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHANKS R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 DR EMBL: Z72502; CAA96584.1; -.
 DR PFAM: PF00201; UDPGT; 1.
 SQ SEQUENCE 586 AA; 67197 MW; DE2A3A87 CRC32;

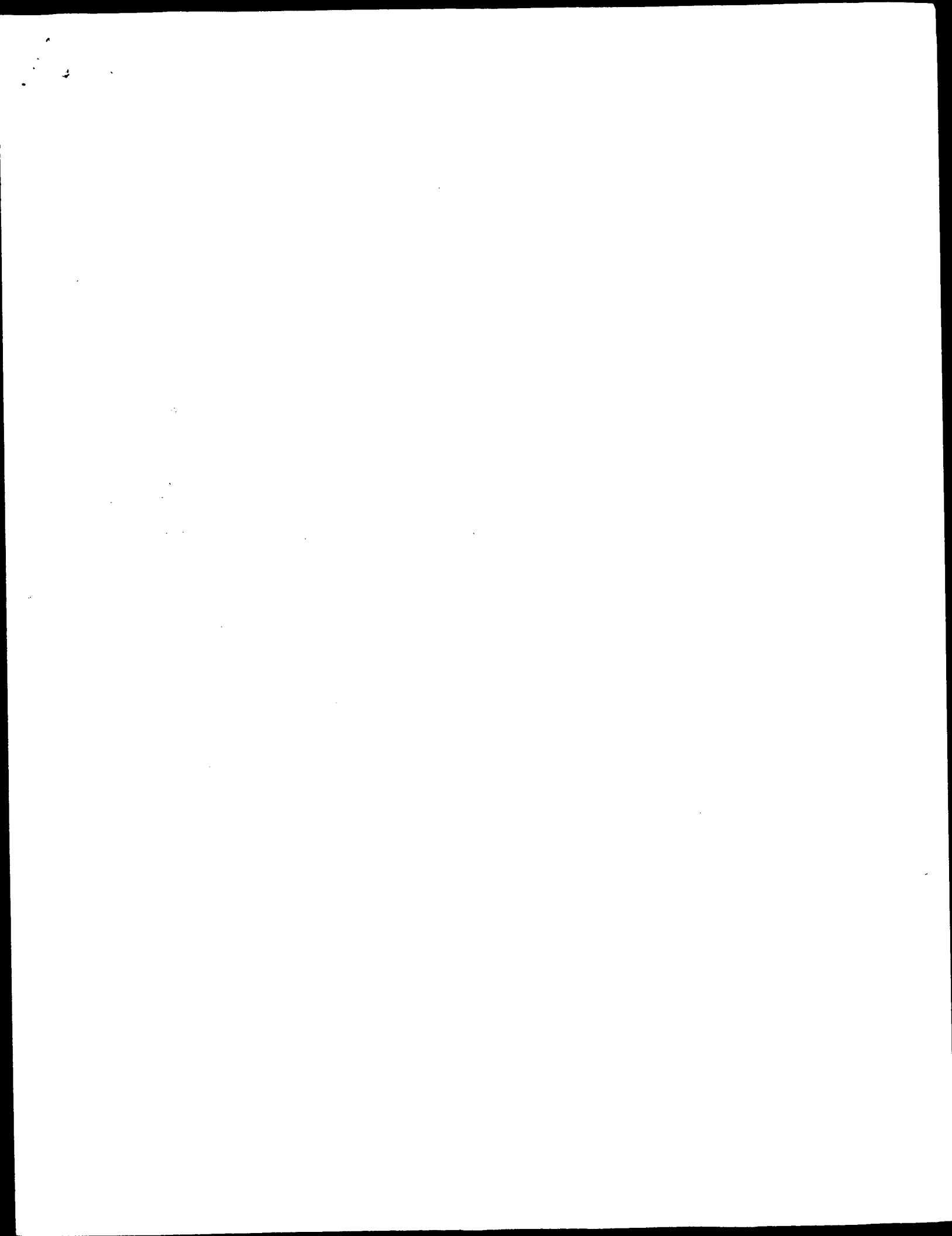
Query Match 15.1%; Score 86; DB 5; Length 586;
 Best Local Similarity 24.5%; Pred. No. 2.36e+00;
 Matches 13; Conservative 21; Mismatches 15; Indels 4; Gaps 4;
 DB 22 KLVV-FNPATGASHNFIKISDILIDAGHDVIMLIPIAMOGKHLVGS-KKV 72

QY 2 KTVAFNCGFGPNRRVFTKRVSNVITH-GRRIDFASKNFHLKNTIGTRI 52
 11: - - - - - 11: - - - - - 11: - - - - -

RESULT 15
 ID 038802; PRELIMINARY; PRT; 802 AA.
 AC 038802;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
 DT 01-NOV-1999 (TRENBLREL. 12, Last annotation update)
 DE ENT-KAURENE SYNTHETASE A.
 GN GAL OR T538.9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 OC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RX MEDLINE: 95086384.
 RA SUN T.P., KAMITA Y.;
 RT "The Arabidopsis GAL locus encodes the cyclase ent-kaurene synthetase
 RT A of gibberellin biosynthesis";
 RL Plant Cell 6:1509-1518(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV COLUMBIA;
 RA DE LA BASTIDE M., GNOU L., HABERMANN K., HUANG E.N., GOTTESMAN T.,
 RA KAPLAN N., LODHI M., JENSEN K., HAMEED A., SCHUTZ K., MARTIENSSEN R.,
 RA KEDDIA N., PARNELL L.D., MCCOMBIE W.R.;
 RT "Arabidopsis thaliana BAC T538 from chromosome IV, short arm";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U11034; AAA53632.1; -.
 DR EMBL: AC004044; AAD13534.1; -.
 DR MENDEL, 7142; Arabid; 1532; 7142.
 DR PFAM: PF01397; Terpene_synth; 1.
 SQ SEQUENCE 802 AA; 93013 MW; 9AA5783B CRC32;

Query Match 15.1%; Score 86; DB 10; Length 802;
 Best Local Similarity 24.0%; Pred. No. 2.36e+00;
 Matches 12; Conservative 18; Mismatches 18; Indels 2; Gaps 2;
 DB 595 ISSSFGSSDSRSFSDFEHYIANARSDHFNDRNMLDPGSGQASR 644
 11: - - - - - 11: - - - - - 11: - - - - -
 QY 3 VTVAFNCGFGPNRRVFTKRVSNVITHGRRIDT-FASKNFHLK-NTIGTR 50

Search completed: Mon Jun 19 15:53:26 2000
 Job time: 19 secs.



WARNING

(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Mpsrch_p protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jun 19 15:57:27 2000; MasPar time 4.99 Seconds

Tabular output not generated. 379.415 Million cell updates/sec

Title: >US-09-142-524A-1
Description: (1-80) from US09142524A.pep
Perfect Score: 569

Sequence: 1 MKVTVAFNQFGPNRRVFIKR.....IASRRVDGIIAAAYONPASWK 80

Scoring table: PAM 150
Gap 11

Searched: 188963 segs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries
Maximum DB seq length 80

Database: a-censseq35
Kgeneseqp

Statistics: Mean 27.708; Variance 116.071; scale 0.239

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
	1	569	100.0	80	1	W27369	Multi-epitope peptide	5.38e-45
	2	128	22.5	47	1	W80357	Sugi allergen protein	7.58e-03
	3	117	20.6	17	1	W80347	Sugi allergen protein	6.45e-02
	4	117	20.6	33	1	W80339	Sugi allergen protein	6.45e-02
	5	115	20.2	17	1	W80345	Sugi allergen protein	9.47e-02
	6	111	19.5	17	1	W80345	Sugi allergen protein	2.03e-01
	7	111	19.5	17	1	R81582	Cedar pollen allergen	2.03e-01
	8	107	18.8	15	1	R81580	Cedar pollen allergen	4.34e-01
	9	107	18.8	15	1	R81580	Cedar pollen allergen	4.34e-01
	10	107	18.8	15	1	W57760	Japan cedar pollen mat	4.34e-01
	11	106	18.6	47	1	W80350	Sugi allergen protein	5.24e-01
	12	103	18.1	35	1	W80342	Sugi allergen protein	9.20e-01
	13	98	17.2	15	1	W57764	Residues 186-200 of Cr	2.33e+00
	14	98	17.2	15	1	R97908	Japan cedar pollen mat	2.33e+00
	15	98	17.2	15	1	R97907	Japan cedar pollen mat	2.33e+00
	16	98	17.2	15	1	W57763	Residues 181-195 of Cr	2.33e+00
	17	97	17.0	30	1	R45588	Cry j I pollen allergen	2.80e+00
	18	95	16.7	15	1	W57755	Residues 211-225 of Cr	4.03e+00
	19	95	16.7	15	1	R89293	Japanese cedar pollen	4.03e+00
	20	95	16.7	17	1	W80349	Sugi allergen protein	4.03e+00
	21	95	16.7	20	1	R45563	Cry j I pollen allergen	4.03e+00
	22	95	16.7	20	1	R82512	Cry j I Japanese Cedar	4.03e+00

23 95 16.7 26 1 R45594 Cry j I pollen allergen 4.03e+00
24 95 16.7 28 1 R45590 Cry j I pollen allergen 4.03e+00
25 95 16.7 30 1 W44687 T-cell epitope peptide 4.03e+00

Note: Post-processor removed 20 summaries from list due to search parameters chosen.

ALIGNMENTS

RESULT 1
ID W27369 standard; peptide: 80 AA.
AC W27369:
DE 24-MAR-1998 (first entry)
DE Multi-epitope peptide used as immunotherapeutic agent #1.
KW Multi-epitope peptide; immunotherapeutic agent; allergic disease;
OS T-cell epitope region; allergen; lymphocyte; immunoglobulin E.
PN W09732600-A1.
PD 12-SEP-1997.
PR 10-MAR-1997; J00740.
PI (MEIP) MEIJI MILK PROD CO LTD.
PI Dairiki K, Iwama A, Kuno K, Kume A, Sone T;
DR WPI: 97-470495/43.
PT Peptide immuno:therapeutic agent to treat allergic diseases -
PT contains multi-epitope peptide containing T cell epitope regions
PS Claim 6; Page 31; 58pp; Japanese.
CC The present sequence represents a multi-epitope peptide which is used as
CC or more different allergens (preferably linked via arginine or lysine
CC dimers), where the T cell epitope regions have a positivity index
CC greater than 100 as measured in a patient group responding to the
CC allergen; have at least 70% reactivity with lymphocytes from patients
CC responding to the allergen; and are not reactive with immunoglobulin E
CC (IGE) antibodies from patients responsive to the allergen. The agent can
CC be used to prevent and treat a wide variety of allergic diseases, e.g. by
CC desensitisation. Side effects, e.g. those mediated by IGE, are reduced.
SQ Sequence 80 AA:

Query Match 100.0%; Score 569; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 5.38e-45;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 MKVTVAFNQFGPNRRVFIKRVSNIHGRRIDIFASKNFKLQNTIGTRISLKTSGK 60
QY 1 MKVTVAFNQFGPNRRVFIKRVSNIHGRRIDIFASKNFKLQNTIGTRISLKTSGK 60

Db 61 IASRRVDGIIAAAYONPASWK 80
QY 61 IASRRVDGIIAAAYONPASWK 80

RESULT 2
ID W80357 standard; peptide: 47 AA.
AC W80357:
DE 11-JAN-1999 (first entry)
DE Sugi allergen protein Cryj1 derived epitope for T cells.
KW T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;
OS Sugi-pollinosis; allergic reaction; pollen.
PN J10259198-A.
PD 29-SEP-1998.
PR 22-DEC-1997; 353448.
PI (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
PI (SANT) SANKYO CO LTD.
PI WPI: 98-577037/49.
PT A linked T cell epitope peptide - used for the treatment of
PT Sugi-pollinosis
PS Claim 10; Page 5; 21pp; Japanese.
CC W80339-58 represent epitopes for T cells, derived from the sugi allergen
CC proteins Cryj1 (W80339-44), W80350-53 and W80356-58) and Cryj2 (W80345-49

Db 1 KVDGIIAAYONPASMWK 16
 :|||||
 QY 65 RVDGIIAAYONPASMWK 80

RESULT 7
 ID R81580 standard; peptide; 17 AA.
 AC R81580;
 DT 24-MAY-1996 (first entry)
 DE Cedar pollen allergen peptide 8 (T-cell epitope).
 KW Cedar; Cryptomeria japonica; pollen; allergen; immunoglobulin E;
 KM IGE; T-cell epitope; antibody; pollinosis; therapy; immunotherapy.
 OS Synthetic.
 PN EP-700929-A2.
 PD 13-MAR-1996.
 PE 08-SEP-1995; 306295.
 PR 10-SEP-1994; JP-242137.
 PR 14-JUL-1995; JP-200221.
 PR 14-JUL-1995; JP-200204.
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Hino K, Saito S, Taniguchi Y.
 DR WPI: 96-140976/15.
 PT New peptide(s) derived from cedar pollen allergens - activate
 PT allergen-specific T-cells, but not allergen-specific IGE antibodies,
 PT used for treating cedar pollinosis
 PS Claim 4; Page 28; 36pp; English.
 CC Synthetic peptides based on portions of cedar pollen allergens A
 CC (R81586) and B (R81587) were tested for their ability to activate
 CC cedar allergen-specific T-cells, but not allergen-specific IGE
 CC antibodies. 6 Peptides (R81580-R81585) were identified as T-cell
 CC epitopes. These peptides, plus subsequences (R81573-79) essential
 CC for T-cell recognition, and homologous peptides (R81588-96) can
 CC be used as immunotherapeutic agents to treat or prevent cedar
 CC pollinosis, avoiding side-effects such as anaphylaxis.
 SQ Sequence 17 AA;

Query Match 19.5%; Score 111; DB 1; Length 17;
 Best Local Similarity 93.8%; Pred. No. 2.03e-01;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 KVDGIIAAYONPASMWK 16
 :|||||
 QY 65 RVDGIIAAYONPASMWK 80

RESULT 8
 ID R97884 standard; peptide; 15 AA.
 AC R97884;
 DT 16-AUG-1996 (first entry)
 DE Japan cedar pollen mature allergen Cry j II amino acids 66-80.
 KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
 KW Sugi pollinosis; diagnosis; treatment.
 OS Cryptomeria japonica.
 PN J08047392-A.
 PD 20-FEB-1996.
 PE 07-NOV-1994; 297840.
 PR 05-NOV-1993; JP-276773.
 PR 26-MAY-1994; JP-134868.
 PA (MEIP) MEIJI MILK PROD CO LTD.
 DR WPI: 96-166249/17.
 PT Japan cedar pollen allergen Cry j II epitope - comprises at least
 PT part of specified 460 amino acid protein
 PS Claim 8; Fig 3; 17pp; Japanese.
 CC R97871-R97960 are overlapping peptides used for the epitope mapping
 CC of the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
 CC peptides of it are useful in the diagnosis, prevention and treatment
 CC of Sugi pollinosis, the allergic reaction to Japan cedar pollen.
 CC Significant regions of the allergen were identified using the
 CC overlapping peptides of the full epitope derived from a Cry j II
 CC antigen-specific T cell line. Amino acids 66-80 (R97884) and 186-200
 CC (R978808) of the full mature 460 amino acid allergen are the most
 CC allergenic of the 90 peptides tested.

SQ Sequence 15 AA;

Query Match 18.8%; Score 107; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.34e-01;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 VDGIIAAYONPASMWK 15
 :|||||
 QY 66 VDGIIAAYONPASMWK 80

RESULT 9
 ID W57760 standard; peptide; 15 AA.
 AC W57760;
 DT 17-SEP-1998 (first entry)
 DE Residues 66-80 of Cry j 2.
 KW Cry j 2; Japanese cedar pollen antigen; allergy; immunotherapy;
 KW HLA class II molecule.
 OS Cryptomeria japonica.
 PN W09820902-A1.
 PD 22-MAY-1998.
 PE 12-NOV-1997; J04129.
 PR 13-NOV-1996; JP-302053.
 PA (MEIP) MEIJI MILK PROD CO LTD.
 PI Dairiki K, Kuno K, Kume A, Sone T;
 DR WPI: 98-297617/26.
 PT Peptides derived from Japanese cedar pollen antigens are
 PT immunotherapeutic agents - useful for allergy treatment and typing
 PT HLA class II molecules in allergy sufferers
 PS Claim 12; Page 30; 50pp; Japanese.
 CC This sequence represents residues 66-80 of the Cry j 2 protein, and
 CC is a peptide of the invention. The peptides are derived from Japanese
 CC cedar pollen antigens, and are used as immunotherapeutic agents in the
 CC treatment of allergy. The peptides can be used for identification and
 CC typing of the particular HLA class II molecules in an allergy sufferer,
 CC and also for peptide immunotherapy of an allergy. Using these peptides
 CC the immunotherapy can be targeted more specifically to the requirements
 CC of the individual patient, allowing more effective treatment of an
 CC allergy, including those patients for whom treatment with a conventional
 CC immunotherapeutic agent is ineffective.
 SQ Sequence 15 AA;

Query Match 18.8%; Score 107; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 4.34e-01;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 VDGIIAAYONPASMWK 15
 :|||||
 QY 66 VDGIIAAYONPASMWK 80

RESULT 10
 ID W80350 standard; peptide; 47 AA.
 AC W80350;
 DT 11-JAN-1999 (first entry)
 DE Sugi allergen protein Cryj1 derived epitope for T cells.
 KW T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;
 KW Sugi-pollinosis; allergic reaction; pollen.
 OS Synthetic.
 PN J10259198-A.
 PD 29-SEP-1998.
 PE 22-DEC-1997; 353448.
 PR 24-DEC-1996; JP-343441.
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PA (SANY) SANKYO CO LTD.
 DR WPI: 98-577037/49.
 PT A linked T cell epitope peptide - used for the treatment of
 PT Sugi-pollinosis
 PS Claim 10; Page 5; 21pp; Japanese.
 CC W80339-58 represent epitopes for T cells, derived from the sugi allergen
 CC proteins Cryj1 (W80339-44; W80350-53 and W80356-58) and Cryj2 (W80345-49
 CC and W80354-55). The peptides are useful for the treatment of
 CC sugi-pollinosis, an allergic reaction of the body to pollen.

SQ Sequence 47 AA:

Query Match 18.8%; Score 107; DB 1; Length 47;

Best Local Similarity 65.6%; Pred. No. 4,34e-01;

Matches 21; Conservative 4; Mismatches 5; Indels 2; Gaps 2;

Db 13 FASKNFHLQKNTMKTVAENQFKITSGKIAS 44

Oy 34 FASKNFHLQKNTIGTGRIS-L-KITSGKIAS 63

RESULT 11

ID W80356 standard; peptide; 47 AA.

AC W80356;

DT 11-JAN-1999 (first entry)

DE Sugi allergen protein Cryj1 derived epitope for T cells.

KW T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;

KM sugi-pollinosis; allergic reaction; pollen.

OS Synthetic.

PN J10259198-A.

PD 29-SEP-1998.

PE 22-DEC-1997; 353448.

PR 24-DEC-1996; JP-343441.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PW (SANT) SANKYO CO LTD.

WPI: 98-57703/49.

PT A linked T cell epitope peptide - used for the treatment of

PS Sugi-pollinosis

PS Claim 10; Page 5; 21pp; Japanese.

CC W80339-58 represent epitopes for T cells, derived from the sugi allergen

CC proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345-49

CC and W80354-55). The peptides are useful for the treatment of

CC sugi-pollinosis, an allergic reaction of the body to pollen.

SQ Sequence 47 AA;

Query Match 18.6%; Score 106; DB 1; Length 47;

Best Local Similarity 69.7%; Pred. No. 5,24e-01;

Matches 23; Conservative 2; Mismatches 5; Indels 3; Gaps 2;

Db 1 FASKNFHLQKNTGIIAAYONPASKYITSGKIAS 33

Oy 34 FASKNFHLQKNT-IGT-GRISLKITSGKIAS 63

RESULT 12

ID W80342 standard; peptide; 35 AA.

AC W80342;

DT 11-JAN-1999 (first entry)

DE Sugi allergen protein Cryj1 derived epitope for T cells.

KW T cell epitope; sugi allergen proteins Cryj1; Cryj2; treatment;

KM sugi-pollinosis; allergic reaction; pollen.

OS Synthetic.

PN J10259198-A.

PD 29-SEP-1998.

PE 22-DEC-1997; 353448.

PR 24-DEC-1996; JP-343441.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PW (SANT) SANKYO CO LTD.

WPI: 98-57703/49.

PT A linked T cell epitope peptide - used for the treatment of

PS Sugi-pollinosis

PS Claim 10; Page 5; 21pp; Japanese.

CC W80339-58 represent epitopes for T cells, derived from the sugi allergen

CC proteins Cryj1 (W80339-44, W80350-53 and W80356-58) and Cryj2 (W80345-49

CC and W80354-55). The peptides are useful for the treatment of

CC sugi-pollinosis, an allergic reaction of the body to pollen.

SQ Sequence 35 AA;

Query Match 18.1%; Score 103; DB 1; Length 35;

Best Local Similarity 66.7%; Pred. No. 9,20e-01;

Matches 22; Conservative 2; Mismatches 6; Indels 3; Gaps 2;

Db 1 FASKNFHLQKNTGIIAAYONPASKYITSGKIAS 33

Oy 34 FASKNFHLQKNT-IGT-GRISLKITSGKIAS 63

RESULT 13

ID W57764 standard; peptide; 15 AA.

AC W57764;

DT 17-SEP-1998 (first entry)

DE Residues 186-200 of Cry j 2.

KW Cry j 2; Japanese cedar pollen antigen; allergy; immunotherapy;

KM HLA class II molecule.

OS Cryptomeria japonica.

PN W06820902-A1.

PD 22-MAY-1998.

PE 12-NOV-1997; J04129.

PR 13-NOV-1996; JP-302053.

PA (MEIP) MEIJI MILK PROD CO LTD.

PW Dairiki K, Kuno K, Kume A, Sone T;

WPI: 98-297617/26.

PT Peptides derived from Japanese cedar pollen antigens are

PT Immunotherapeutic agents - useful for allergy treatment and typing

PT HLA Class II molecules in allergy sufferers

PS Claim 12; Page 31; 50pp; Japanese.

CC This sequence represents residues 186-200 of the Cry j 2 protein, and

CC is a peptide of the invention. The peptides are derived from Japanese

CC cedar pollen antigens, and are used as immunotherapeutic agents in the

CC treatment of allergy. The peptides can be used for identification and

CC typing of the particular HLA class II molecules in an allergy sufferer,

CC and also for peptide immunotherapy of an allergy. Using these peptides

CC the immunotherapy can be targeted more specifically to the requirements

CC of the individual patient, allowing more effective treatment of an

CC allergy, including those patients for whom treatment with a conventional

SQ immunotherapeutic agent is ineffective.

Sequence 15 AA;

Query Match 17.2%; Score 98; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 2,33e-00;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ASKNFHLQKNTIGTG 15

Oy 35 ASKNFHLQKNTIGTG 49

RESULT 14

ID R97908 standard; peptide; 15 AA.

AC R97908;

DT 16-AUG-1996 (first entry)

DE Japan cedar pollen mature allergen Cry j II amino acids 186-200.

KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;

KM sugi pollinosis; diagnosis; treatment.

OS Cryptomeria japonica.

PN J08047392-A.

PD 20-FEB-1996.

PE 07-NOV-1994; 297840.

PR 05-NOV-1993; JP-276773.

PW 26-MAY-1994; JP-134868.

PA (MEIP) MEIJI MILK PROD CO LTD.

WPI: 96-166249/17.

PT Japan cedar pollen allergen Cry j II epitope - comprises at least

PT part of specified 460 amino acid protein

PS Claim 8; Fig 4; 17pp; Japanese.

CC R97871-R97960 are overlapping peptides used for the epitope mapping

CC of the Japan cedar pollen allergen Cry j II. Cry j II and allergenic

CC peptides of it are useful in the diagnosis, prevention and treatment

CC of sugi pollinosis, the allergic reaction to Japan cedar pollen.

CC Significant regions of the allergen were identified using the

CC overlapping peptides of the full epitope derived from a Cry j II

CC antigen-specific T cell line. Amino acids 66-80 (R97884) and 186-200

CC (R978908) of the full mature 460 amino acid allergen are the most

SQ Sequence 15 AA;

Query Match 17.2%; Score 98; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.33e+00;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ASKNFHLQKNTGTG 15
 |||
 QY 35 ASKNFHLQKNTGTG 49

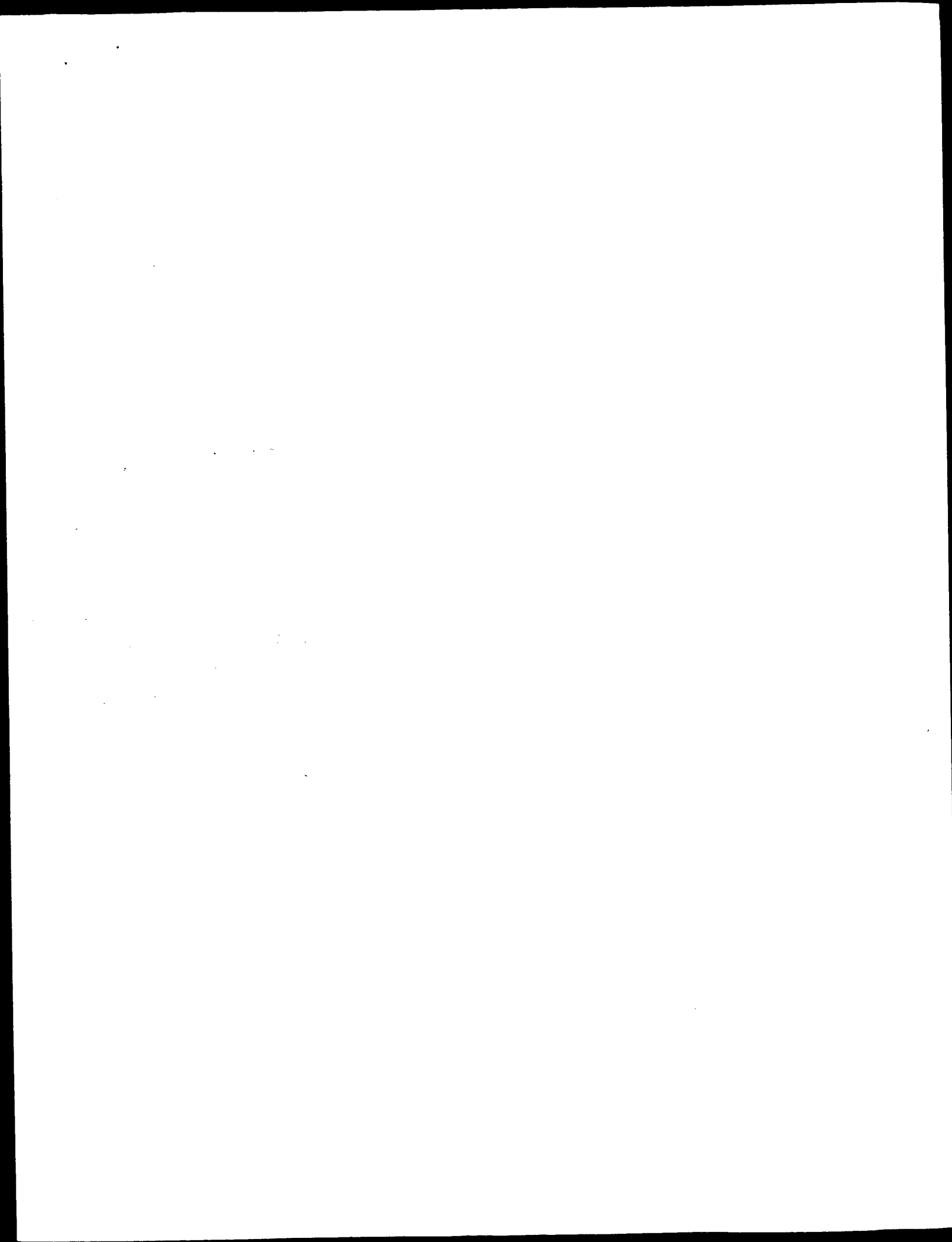
RESULT 15

ID R97907 standard; peptide; 15 AA.
 AC R97907:
 DT 16-AUG-1996 (first entry)
 DE Japan cedar pollen mature allergen Cry j II amino acids 181-195.
 KW Allergen; epitope; overlapping peptide; Cry j II; cedar pollen;
 KM Sugl pollinosis; diagnosis; treatment.
 OS Cryptomeria japonica.
 PN J08047392-A.
 PD 20-FEB-1996:
 PR 07-NOV-1994; 297840.
 PR 05-NOV-1993; JP-276773.
 PR 26-MAY-1994; JP-134868.
 PA (MEIP) MEIJI MILK PROD CO LTD.
 DR WPI; 96-166249/17.
 PT Japan cedar pollen allergen Cry j II epitope - comprises at least
 part of specified 460 amino acid protein
 PS Claim 8; Fig 4; 17pp; Japanese.
 CC R97871-R97960 are overlapping peptides used for the epitope mapping
 of the Japan cedar pollen allergen Cry j II. Cry j II and allergenic
 peptides of it are useful in the diagnosis, prevention and treatment
 CC of Sugl pollinosis, the allergic reaction to Japan cedar pollen.
 CC Significant regions of the allergen were identified using the
 CC overlapping peptides of the full epitope derived from a Cry j II
 CC antigen-specific T cell line. Amino acids 66-80 (R97884) and 186-200
 CC (R978908) of the full mature 460 amino acid allergen are the most
 SQ allergenic of the 90 peptides tested.
 Sequence 15 AA;

Query Match 17.2%; Score 98; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.33e+00;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 IDIFASKNFHLQKN 15
 |||
 QY 31 IDIFASKNFHLQKN 44

Search completed: Mon Jun 19 15:57:41 2000
 Job time : 14 secs.



WIRE (TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Mpsrch.jp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jun 19 15:57:00 2000; MasPar time 9.23 Seconds

Tabular output not generated. 408.972 Million cell updates/sec

Title: >US-09-142-524A-1

Description: (1-80) from US09142524A.pep

Perfect Score: 569

Sequence: 1 MKVTVAFNQFGPNRRVFIKR.....IASRRVDGIIAAYONPASWK 80

Scoring table: PAM 150

Gap 11

Searched: 142080 segs, 47172406 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Maximum DB seq length 80

Database: p1r62

1:p1r1 2:p1r2 3:p1r3 4:p1r4

Statistics: Mean 39.829; Variance 80.867; scale 0.493

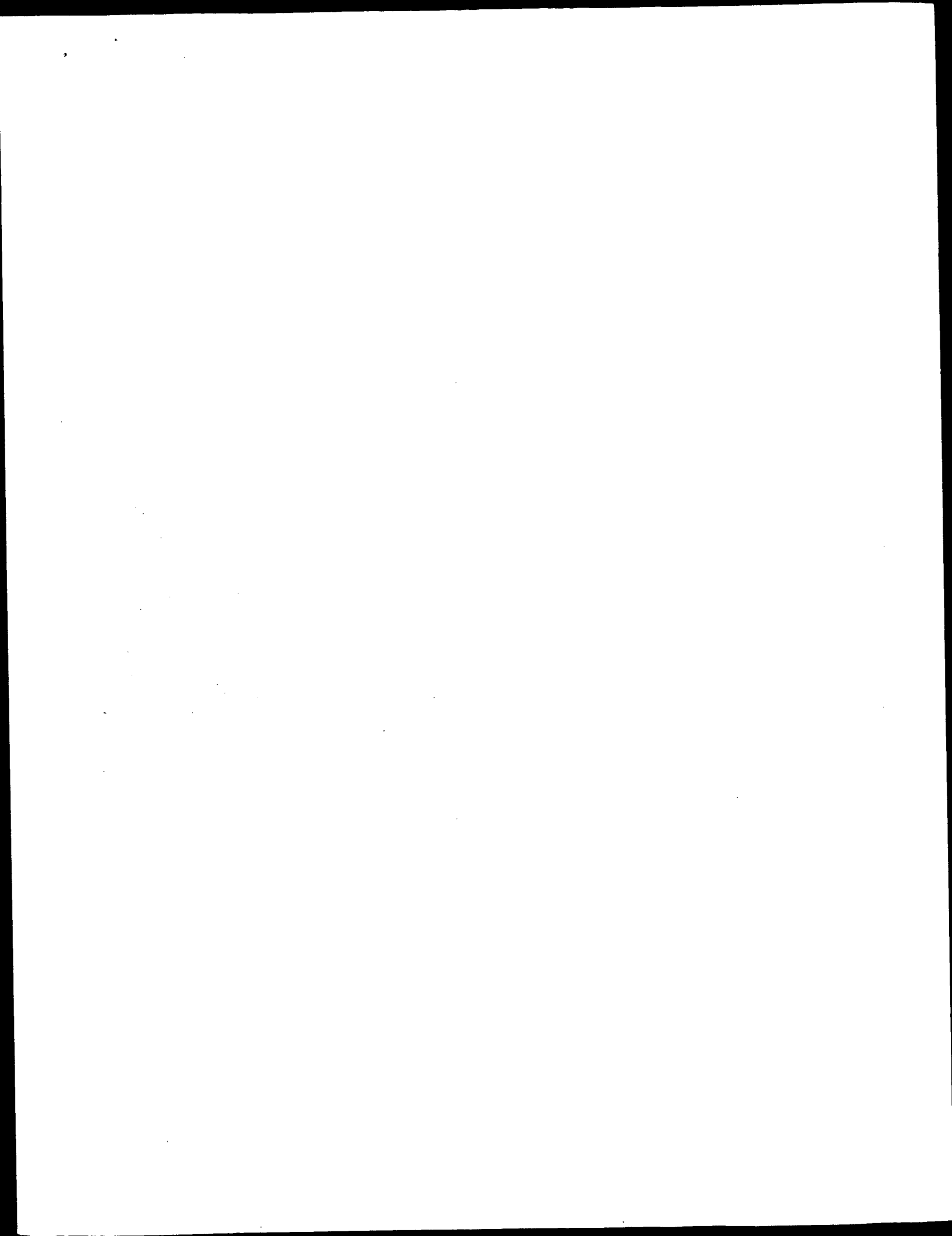
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	No.	Score	Match	Length	DB	ID	Description	Pred.	No.
--------	-------	-----	-------	-------	--------	----	----	-------------	-------	-----

No matches found.

Search completed: Mon Jun 19 15:57:10 2000
Job time : 10 secs.



W P E R L H
(TM)

Release 3.1A John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993-1998 University of Edinburgh, U.K.
Distribution rights by Oxford Molecular Ltd

Mpsrch_dp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jun 19 15:55:43 2000; MasPar time 5.66 Seconds

Tabular output not generated. 430.118 Million cell updates/sec

Title: >US-09-142-524A-1

Description: (1-80) from US09142524A.pep

Perfect Score: 569

Sequence: 1 MKVTVAFNQFGPNRRVFIK.....IASRRVDCIIAAYONPASWK 80

Scoring table: PAM 150
Gap 11

Searched: 83857 seqs, 30454973 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Maximum DB seq length 80

Database: swiss-prot38
1:swissprot

Statistics: Mean 40.706; Variance 73.263; scale 0.556

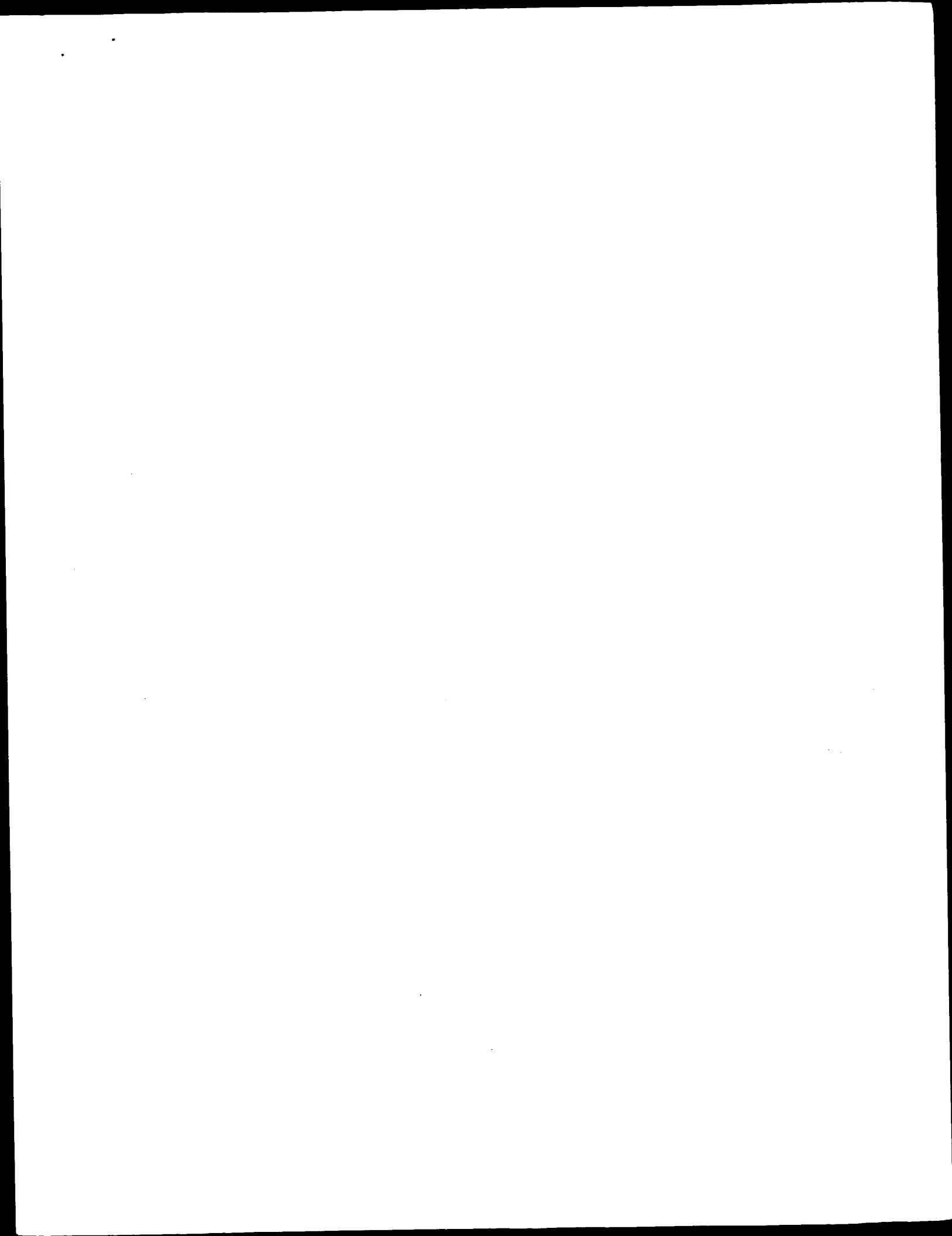
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	
No.	Score	Match length DB ID Description Pred. No.

No matches found.

Search completed: Mon Jun 19 15:56:03 2000
Job time : 20 secs.



WIPERH

(TM)

 Release 3.1A John F. Collins, Biocomputing Research Unit.
 Copyright (c) 1993-1998 University of Edinburgh, U.K.
 Distribution rights by Oxford Molecular Ltd

Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Mon Jun 19 15:56:19 2000; MasPar time 14.21 Seconds

Tabular output not generated. 390.261 Million cell updates/sec

Title: >US-09-142-524A-1

Description: (1-80) from US09142524A.pep

Perfect score: 569

Sequence: 1 MKYVYAFNQFGPNRRVFIKR.....IASRRVDGIIAAYQNPASWK 80

Scoring table: PAM 150

Gap 11

Searched: 225878 segs, 69334122 residues

Post-processing: Minimum Match 08

Listing first 45 summaries

Maximum DB seq length 80

Database:

sptrembl12

1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human

5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle

9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified

13:sp_vertebrate 14:sp_virus

Statistics: Mean 39.247; Variance 71.415; scale 0.550

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	No.	Score	Match	Length	ID	Description	Pred. No.

No matches found.

Search completed: Mon Jun 19 15:56:42 2000
 Job time : 23 secs.

